Serial No.: 08/866,354

Page 11, line 31, after "(rat GRR3)" insert --(SEQ ID NO: 42)--.

Page 12, line 1, after "sequence" insert -(SEQ ID NO: 43)--.

Page 12, line 25, after "consensus sequence" insert -- (SEQ ID NO: 44)--.

Page 98, line 18, after "Figure 26" insert -- (SEQ ID NO: 44)--.

Page 98, line 30, after "Figure 26" insert -- (SEQ ID NO: 44)--.

REMARKS

As described above, the specification has been amended so that the figures are more clearly referenced by the appropriate sequence identification numbers. The amendments are fully supported by the specification, and no new matter has been added.

Respectfully submitted,

David R. Com

Daniel R. Curry

Attorney for Applicants Registration No.: 32,727 Phone: (805) 447-8102

Date: April 6, 1998

Please send all future correspondence to:

U.S. Patent Operations/DRC
Dept. 430, M/S 27-4-A
AMGEN INC.
One Amgen Center Drive
Thousand Oaks, California 91320-1789

45

SEOUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: Fox, Gary M Jing, Shuqian Wen, Duanzhi
 - (ii) TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTORS
 - (iii) NUMBER OF SEQUENCES: 44
 - (iv) CORRESPONDENCE ADDRESS:

 - (A) ADDRESSEE: AMGEN INC(B) STREET: One Amgen Center Drive
 - (C) CITY: Thousand Oaks
 - (D) STATE: CA

 - (E) COUNTRY: US (F) ZIP: 91320-1789
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk

 - (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/866,354
 - (B) FILING DATE: 30-MAY-1997
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/837,199
 - (B) FILING DATE: 14-APR-1997
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/015,907
 - (B) FILING DATE: 22-APR-1996
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/017,221
 - (B) FILING DATE: 09-MAY-1996
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Curry, Daniel R.
 - (B) REGISTRATION NUMBER: 32,727
 - (C) REFERENCE/DOCKET NUMBER: A-401B
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2568 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 540..1934

a

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

								E			00011	JL J.	201111	, DL	(11)	
60	CCCTAA	CATO	CTA A	ACCAC	ATA	rcca	CGCTT	C GCC	rccgo	ATTC	GC C	ACAC	CGGA	CCT (CTGG	AATO
120	TTCGAG	CCCI	rcg (CAACI	GCC	CCTG	CGTO	A AA	rcggz	CTGC	GC T	GAGG	AGCC	CCG 2	CATO	CGA
180	AGATAA	CGC	CTA (TTTC	TCTT	rttt	CTTTT	тто	rTTT'	ATTT	rc T	CGCA'	TAC	AGA 1	rcga/	CTC
240	AATAAG	ATA	AAG A	CTGA	GCC	CATT	ACAC	G GGZ	GCG	AGGG	AG G	GGGA	GAAA	CCG (SAGC	AGT
300	TTGGGT	CAGGT	GTC (rtgac	CGG	CGGT	GACGO	TG	GCAG	CGCC	CC T	GGCT	AACTO	ACA A	AATA	TAA
360	GAGTCG	AGCTO	CGG A	ATCC	GCC	CCTC	CCGC	C TC	CCGC	GGAA	AG C	raaa	CCC	GAA (ACCTO	CGG
420	rgaact	BAGCT	ATG (CTGGA	TCAG	CTT	rtcc:	A GT	CCGG	AGAC	GC C	rgcT(rggc'	CGG 1	GCGG	CCG
480	CGGCAA	CCTC	GCT (CTGAC	ACG	CTGC	ATCG(G GGZ	rccg	GCTGT	AC A	CAGC	AGAG	GCC 2	GCG	TTG
539	GCACC	CCGC	CGC (3CCC(CCA	GGGA	GCG	G GG	rtgg(rrrr:	GA T	rcgg	CGGC'	CGG (CCAG	GAC
587	CTC Leu	TTG Leu 15	GAC Asp	TTG Leu	CTC Leu	CCG Pro	CTG Leu 10	GCG Ala	TTC Phe	TAC Tyr	CTG Leu	ACC Thr 5	GCG Ala	CTG Leu	TTC Phe	ATG Met 1
635	GCC Ala	AAA Lys	GTG Val 30	TGC Cys	GAT Asp	CTG Leu	CGC Arg	GAC Asp 25	GGA Gly	GGC Gly	AGC Ser	GTG Val	GAA Glu 20	GCC Ala	TCG Ser	CTG Leu
683	ACG Thr	CGC Arg	TAC Tyr	AAG Lys 45	ACC Thr	AGC Ser	TGC Cys	AGC Ser	CAG Gln 40	GAG Glu	AAG Lys	CTG Leu	TGC Cys	CAG Gln 35	GAT Asp	AGT Ser
731	TCC Ser	GCA Ala	CTG Leu	AGC Ser	TTC Phe 60	AAC Asn	ACC Thr	GAG Glu	AAG Lys	GGC Gly 55	GCG Ala	GTG Val	TGC Cys	CAG Gln	AGG Arg 50	CTA Leu
779	AAG Lys 80	CTG Leu	GCC Ala	GAG Glu	ATG Met	GCC Ala 75	AGC Ser	CGC Arg	TGC Cys	GAG Glu	GAT Asp 70	AAG Lys	GCC Ala	GAG Glu	CTG Leu	GGC Gly 65
827	GAG Glu	AAG Lys 95	AAG Lys	ATG Met	GGT Gly	CGG Arg	AAG Lys 90	TGC Cys	CGC Arg	TGC Cys	AAC Asn	TAC Tyr 85	CTC Leu	TCG Ser	AAG Lys	CAG Gln
875	GGA Gly	CAG Gln	CTG Leu 110	AGC Ser	CAG Gln	TAC Tyr	ATG Met	AGC Ser 105	TGG Trp	TAC Tyr	ATT Ile	CGC Arg	CTG Leu 100	TGC Cys	AAC Asn	AAG Lys
923	TTG Leu	AGA Arg	AGC Ser	AAC Asn 125	GTT Val	CCA Pro	GAA Glu	TAT Tyr	CCA Pro 120	TCC Ser	GAT Asp	GAG Glu	CTG Leu	CTG Leu 115	GAT Asp	AAT Asn
971	CAA Gln	CAG Gln	TTT Phe	GTT Val	GAT Asp 140	TCA Ser	ATA Ile	TTC Phe	CCA Pro	GTC Val 135	GTG Val	CGG Arg	TTC Phe	ATA Ile	GAT Asp 130	TCA Ser
1019	GCC Ala 160	AAG Lys	GCG Ala	GCA Ala	GAT Asp	CTG Leu 155	TGC Cys	AAC Asn	AAC Asn	GGG Gly	AAA Lys 150	CCC Pro	ATT Ile	CAC His	GAG Glu	GTG Val 145
1067	ACC Thr	ATC Ile	TAC Tyr	GCG Ala	TCG Ser	AGG Arg	TAC Tyr	AAG Lys	AAG Lys	TGC Cys	ATT Ile	GAC Asp	GAC Asp	CTC Leu	AAC Asn	TGC Cys

				165					170					175		
CCG Pro	TGC Cys	ACC Thr	ACC Thr 180	AGC Ser	GTG Val	TCC Ser	AAC Asn	GAT Asp 185	GTC Val	TGC Cys	AAC Asn	CGC Arg	CGC Arg 190	AAG Lys	TGC Cys	1115
CAC His	AAG Lys	GCC Ala 195	CTC Leu	CGG Arg	CAG Gln	TTC Phe	TTT Phe 200	GAC Asp	AAG Lys	GTC Val	CCG Pro	GCC Ala 205	AAG Lys	CAC His	AGC Ser	1163
TAC Tyr	GGA Gly 210	ATG Met	CTC Leu	TTC Phe	TGC Cys	TCC Ser 215	TGC Cys	CGG Arg	GAC Asp	ATC Ile	GCC Ala 220	TGC Cys	ACA Thr	GAG Glu	CGG Arg	1211
AGG Arg 225	CGA Arg	CAG Gln	ACC Thr	ATC Ile	GTG Val 230	CCT Pro	GTG Val	TGC Cys	TCC Ser	TAT Tyr 235	GAA Glu	GAG Glu	AGG Arg	GAG Glu	AAG Lys 240	1259
CCC Pro	AAC Asn	TGT Cys	TTG Leu	AAT Asn 245	TTG Leu	CAG Gln	GAC Asp	TCC Ser	TGC Cys 250	AAG Lys	ACG Thr	AAT Asn	TAC Tyr	ATC 11e 255	TGC Cys	1307
AGA Arg	TCT Ser	CGC Arg	CTT Leu 260	GCG Ala	GAT Asp	TTT Phe	TTT Phe	ACC Thr 265	AAC Asn	TGC Cys	CAG Gln	CCA Pro	GAG Glu 270	TCA Ser	AGG Arg	1355
TCT Ser	GTC Val	AGC Ser 275	AGC Ser	TGT Cys	CTA Leu	AAG Lys	GAA Glu 280	AAC Asn	TAC Tyr	GCT Ala	GAC Asp	TGC Cys 285	CTC Leu	CTC Leu	GCC Ala	1403
TAC Tyr	TCG Ser 290	GGG Gly	CTT Leu	ATT Ile	GGC Gly	ACA Thr 295	GTC Val	ATG Met	ACC Thr	CCC Pro	AAC Asn 300	TAC Tyr	ATA Ile	GAC Asp	TCC Ser	1451
AGT Ser 305	AGC Ser	CTC Leu	AGT Ser	GTG Val	GCC Ala 310	CCA Pro	TGG Trp	TGT Cys	GAC Asp	TGC Cys 315	AGC Ser	AAC Asn	AGT Ser	GGG Gly	AAC Asn 320	1499
GAC Asp	CTA Leu	GAA Glu	GAG Glu	TGC Cys 325	TTG Leu	AAA Lys	TTT Phe	TTG Leu	AAT Asn 330	TTC Phe	TTC Phe	AAG Lys	GAC Asp	AAT Asn 335	ACA Thr	1547
TGT Cys	CTT Leu	AAA Lys	AAT Asn 340	GCA Ala	ATT Ile	CAA Gln	GCC Ala	TTT Phe 345	GGC Gly	AAT Asn	GGC Gly	TCC Ser	GAT Asp 350	GTG Val	ACC Thr	1595
GTG Val	TGG Trp	CAG Gln 355	CCA Pro	GCC Ala	TTC Phe	CCA Pro	GTA Val 360	CAG Gln	ACC Thr	ACC Thr	ACT Thr	GCC Ala 365	ACT Thr	ACC Thr	ACC Thr	1643
ACT Thr	GCC Ala 370	CTC Leu	CGG Arg	GTT Val	AAG Lys	AAC Asn 375	AAG Lys	CCC Pro	CTG Leu	GGG Gly	CCA Pro 380	GCA Ala	GGG Gly	TCT Ser	GAG Glu	1691
AAT Asn 385	GAA Glu	ATT Ile	CCC Pro	ACT Thr	CAT His 390	GTT Val	TTG Leu	CCA Pro	CCG Pro	TGT Cys 395	GCA Ala	AAT Asn	TTA Leu	CAG Gln	GCA Ala 400	1739
CAG Gln	AAG Lys	CTG Leu	AAA Lys	TCC Ser 405	AAT Asn	GTG Val	TCG Ser	GGC Gly	AAT Asn 410	ACA Thr	CAC His	CTC Leu	TGT Cys	ATT Ile 415	TCC Ser	1787
AAT Asn	GGT Gly	AAT Asn	TAT Tyr	GAA Glu	AAA Lys	GAA Glu	GGT Gly	CTC Leu	GGT Gly	GCT Ala	TCC Ser	AGC Ser	CAC His	ATA Ile	ACC Thr	1835

	420		425	430	
ACA AAA TC Thr Lys Se 43	r Met Ala A	GCT CCT CCA Ala Pro Pro 440	AGC TGT GGT Ser Cys Gly	CTG AGC CCA CTG Leu Ser Pro Leu 445	CTG 1883 Leu
GTC CTG GT Val Leu Va 450	G GTA ACC (l Val Thr A	GCT CTG TCC Ala Leu Ser 455	ACC CTA TTA Thr Leu Leu	TCT TTA ACA GAA Ser Leu Thr Glu 460	ACA 1931 Thr
TCA TAGCTG Ser 465	CATT AAAAA	AATAC AATATO	GGACA TGTAAA	AAGA CAAAAACCAA	1984
GTTATCTGTT	TCCTGTTCTC	C TTGTATAGCT	T GAAATTCCAG	TTTAGGAGCT CAGT	TGAGAA 2044
ACAGTTCCAT	TCAACTGGAA	A CATTTTTTT	TTTNCCTTTT	AAGAAAGCTT CTTG	TGATCC 2104
TTNGGGGCTT	CTGTGAAAA	A CCTGATGCAC	G TGCTCCATCC	AAACTCAGAA GGCT	TTGGGA 2164
TATGCTGTAT	TTTAAAGGG	A CAGTTTGTA	A CTTGGGCTGT	AAAGCAAACT GGGG	CTGTGT 2224
TTTCGATGAT	GATGATNATO	C ATGATNATGA	A TNNNNNNNN	NNNNNNNNN NNNN	NNNNNN 2284
NNNNNNNNN	GATTTTAAC	A GTTTTACTTO	C TGGCCTTTCC	TAGCTAGAGA AGGA	.GTTAAT 2344
ATTTCTAAGG	TAACTCCCA	r atctccttt	A ATGACATTGA	TTTCTAATGA TATA	AATTTC 2404
AGCCTACATT	GATGCCAAG	C TTTTTTGCC	A CAAAGAAGAT	TCTTACCAAG AGTG	GGCTTT 2464
GTGGAAACAG	CTGGTACTG	A TGTTCACCT	r tatatatgta	CTAGCATTTT CCAC	GCTGAT 2524
GTTTATGTAC	TGTAAACAG	r TCTGCACTC	r TGTACAAAAG	AAAA	2568
(2) INFORM	ATION FOR	SEQ ID NO:2:	:		
(i)	(A) LENG (B) TYPI	CHARACTERIST GTH: 465 ami E: amino aci OLOGY: linea	ino acids id		
(ii)	MOLECULE '	TYPE: protei	in		
(xi)	SEQUENCE I	DESCRIPTION	: SEQ ID NO:	2:	
Met Phe Le 1	u Ala Thr 1 5	Leu Tyr Phe	Ala Leu Pro 10	Leu Leu Asp Leu 15	Leu
Leu Ser Al	a Glu Val : 20	Ser Gly Gly	Asp Arg Leu 25	Asp Cys Val Lys	Ala
Ser Asp Gl	n Cys Leu	Lys Glu Gln		Thr Lys Tyr Arg	Thr

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser 50 55 60

Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys 65 70 75 80

Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu 85 90 95

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln 135 Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys 185 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys 230 Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala 280 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu

445 440 Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr 460 455 Ser 465 (2) INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2138 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 302..1705 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: AGCTCGCTCT CCCGGGGCAG TGGTGTGGAT GCACCGGAGT TCGGGCGCTG GGCAAGTTGG 60 GTCGGAACTG AACCCCTGAA AGCGGGTCCG CCTCCCGCCC TCGCGCCCGC CCGGATCTGA 120 GTCGCTGGCG GCGGTGGGCG GCAGAGCGAC GGGGAGTCTG CTCTCACCCT GGATGGAGCT 180 GAACTTTGAG TGGCCAGAGG AGCGCAGTCG CCCGGGGATC GCTGCACGCT GAGCTCTCTC 240 300 CCCGAGACCG GGCGGCGGT TTGGATTTTG GGGGGGCGGG GACCAGCTGC GCGGCGGCAC C ATG TTC CTA GCC ACT CTG TAC TTC GCG CTG CCA CTC CTG GAT TTG Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu 346 CTG ATG TCC GCC GAG GTG AGT GGT GGA GAC CGT CTG GAC TGT GTG AAA 394 Leu Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys GCC AGC GAT CAG TGC CTG AAG GAA CAG AGC TGC AGC ACC AAG TAC CGC Ala Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg 442 35 ACA CTA AGG CAG TGC GTG GCG GGC AAG GAA ACC AAC TTC AGC CTG ACA 490 Thr Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr 50 TCC GGC CTT GAG GCC AAG GAT GAG TGC CGT AGC GCC ATG GAG GCC TTG 538 Ser Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu AAG CAG AAG TCT CTG TAC AAC TGC CGC TGC AAG CGG GGC ATG AAG AAA 586 Lys Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys

GAG AAG AAT TGT CTG CGT ATC TAC TGG AGC ATG TAC CAG AGC CTG CAG

Glu Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln

100

105

634

GGA Gly	AAT Asn	GAC Asp	CTC Leu 115	CTG Leu	GAA Glu	GAT Asp	TCC Ser	CCG Pro 120	TAT Tyr	GAG Glu	CCG Pro	GTT Val	AAC Asn 125	AGC Ser	AGG Arg	682
TTG Leu	TCA Ser	GAT Asp 130	ATA Ile	TTC Phe	CGG Arg	GCA Ala	GTC Val 135	CCG Pro	TTC Phe	ATA Ile	TCA Ser	GAT Asp 140	GTT Val	TTC Phe	CAG Gln	730
CAA Gln	GTG Val 145	GAA Glu	CAC His	ATT Ile	TCC Ser	AAA Lys 150	GGG Gly	AAC Asn	AAC Asn	TGC Cys	CTG Leu 155	GAC Asp	GCA Ala	GCC Ala	AAG Lys	778
GCC Ala 160	TGC Cys	AAC Asn	СТG Leu	GAC Asp	GAC Asp 165	ACC Thr	TGT Cys	AAG Lys	AAG Lys	TAC Tyr 170	AGG Arg	TCG Ser	GCC Ala	TAC Tyr	ATC Ile 175	826
ACC Thr	CCC Pro	TGC Cys	ACC Thr	ACC Thr 180	AGC Ser	ATG Met	TCC Ser	AAC Asn	GAG Glu 185	GTC Val	TGC Cys	AAC Asn	CGC Arg	CGT Arg 190	AAG Lys	874
TGC Cys	CAC His	AAG Lys	GCC Ala 195	CTC Leu	AGG Arg	CAG Gln	TTC Phe	TTC Phe 200	GAC Asp	AAG Lys	GTT Val	CCG Pro	GCC Ala 205	AAG Lys	CAC His	922
AGC Ser	TAC Tyr	GGG Gly 210	ATG Met	CTC Leu	TTC Phe	TGC Cys	TCC Ser 215	TGC Cys	CGG Arg	GAC Asp	ATC Ile	GCC Ala 220	TGC Cys	ACC Thr	GAG Glu	970
CGG Arg	CGG Arg 225	CGA Arg	CAG Gln	ACT Thr	ATC Ile	GTC Val 230	CCC Pro	GTG Val	TGC Cys	TCC Ser	TAT Tyr 235	GAA Glu	GAA Glu	CGA Arg	GAG Glu	1018
AGG Arg 240	CCC Pro	AAC Asn	TGC Cys	CTG Leu	AGT Ser 245	CTG Leu	CAA Gln	GAC Asp	TCC Ser	TGC Cys 250	AAG Lys	ACC Thr	AAT Asn	TAC Tyr	ATC Ile 255	1066
TGC Cys	AGA Arg	TCT Ser	CGC Arg	CTT Leu 260	GCA Ala	GAT Asp	TTT Phe	TTT Phe	ACC Thr 265	AAC Asn	TGC Cys	CAG Gln	CCA Pro	GAG Glu 270	TCA Ser	1114
AGG Arg	TCT Ser	GTC Val	AGC Ser 275	AAC Asn	TGT Cys	CTT Leu	AAG Lys	GAG Glu 280	AAC Asn	TAC Tyr	GCA Ala	GAC Asp	TGC Cys 285	CTC Leu	CTG Leu	1162
GCC Ala	TAC Tyr	TCG Ser 290	GGA Gly	CTG Leu	ATT Ile	GGC Gly	ACA Thr 295	GTC Val	ATG Met	ACT Thr	CCC Pro	AAC Asn 300	TAC Tyr	GTA Val	GAC Asp	1210
TCC Ser	AGC Ser 305	AGC Ser	CTC Leu	AGC Ser	GTG Val	GCA Ala 310	CCA Pro	TGG Trp	TGT Cys	GAC Asp	TGC Cys 315	AGC Ser	AAC Asn	AGC Ser	GGC Gly	1258
AAT Asn 320	GAC Asp	CTG Leu	GAA Glu	GAC Asp	TGC Cys 325	TTG Leu	AAA Lys	TTT Phe	CTG Leu	AAT Asn 330	TTT Phe	TTT Phe	AAG Lys	GAC Asp	AAT Asn 335	1306
ACT Thr	TGT Cys	CTC Leu	AAA Lys	AAT Asn 340	GCA Ala	ATT Ile	CAA Gln	GCC Ala	TTT Phe 345	GGC Gly	AAT Asn	GGC Gly	TCA Ser	GAT Asp 350	GTG Val	1354
ACC Thr	ATG Met	TGG Trp	CAG Gln 355	CCA Pro	GCC Ala	CCT Pro	CCA Pro	GTC Val 360	CAG Gln	ACC Thr	ACC Thr	ACT Thr	GCC Ala 365	ACC Thr	ACT Thr	1402

ACC Thr	ACT Thr	GCC Ala 370	TTC Phe	CGG Arg	GTC Val	AAG Lys	AAC Asn 375	AAG Lys	CCT Pro	CTG Leu	GGG Gly	CCA Pro 380	GCA Ala	GGG Gly	TCT Ser	1450)
GAG Glu	AAT Asn 385	GAG Glu	ATC Ile	CCC Pro	ACA Thr	CAC His 390	GTT Val	TTA Leu	CCA Pro	CCC Pro	TGT Cys 395	GCG Ala	AAT Asn	TTG Leu	CAG Gln	1498	3
GCT Ala 400	CAG Gln	AAG Lys	CTG Leu	AAA Lys	TCC Ser 405	AAT Asn	GTG Val	TCG Ser	GGT Gly	AGC Ser 410	ACA Thr	CAC His	CTC Leu	TGT Cys	CTT Leu 415	1546	;
TCT Ser	GAT Asp	AGT Ser	GAT Asp	TTC Phe 420	GGA Gly	AAG Lys	GAT Asp	GGT Gly	CTC Leu 425	GCT Ala	GGT Gly	GCC Ala	TCC Ser	AGC Ser 430	CAC His	1594	Ŀ
ATA Ile	ACC Thr	ACA Thr	AAA Lys 435	TCA Ser	ATG Met	GCT Ala	GCT Ala	CCT Pro 440	CCC Pro	AGC Ser	TGC Cys	AGT Ser	CTG Leu 445	AGC Ser	TCA Ser	1642	?
CTG Leu	CCG Pro	GTG Val 450	CTG Leu	ATG Met	CTC Leu	ACC Thr	GCC Ala 455	CTT Leu	GCT Ala	GCC Ala	CTG Leu	TTA Leu 460	TCT Ser	GTA Val	TCG Ser	1690)
			ACG Thr		TAGO	CTGCA	ATC C	CGGGA	AAAC	A GI	TATGA	AAAC	ACA	AAAG	SAGA	1745	;
ACC	AAGTA	ATT (CTGTC	CCTC	T CC	тстт	GTAT	' ATC	TGA	AAT	CCAC	TTTT	'AA A	AAGCI	CCGTT	1805	ذ
GAG	AAGCA	GT T	TCAC	CCA	AC TO	GAAC	TCTI	TCC	TTGT	TTT	TAAG	SAAAG	CT T	rgrge	SCCCTC	1865	5
AGG	GCTI	CT (STTGA	AGAZ	AC TO	CTAC	AGGG	G CTA	OTTA	CAA	ACCO	ATA	AGG (CTCTC	GGGCG	1925	;
TGGT	rgcgc	CT T	raago	GGAC	CC AT	TTGC	ACCA	TGI	AAA	CAA	GCTG	GGCI	TA T	CATO	TGTTT	1985	;
GATO	GTGA	GG A	ATGGI	AGTO	G TO	SATGA	TGAT	GG1	TTAAT	ATT	ACAG	CTT	AA (CCTC	TTCTC	2045	;
TCT	ACTGO	TT A	AGGAA	CAG	SA GA	TACI	'ATTG	ATA	AAGA	TTC	TTCC	CATGI	CT T	PACTO	CAGCAG	2105	;
CATT	rgcci	TC T	rgaac	ACAC	G CC	CCGCA	GCC	TCG	}							2138	}

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 468 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu 1 5 10 15

Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala 20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr 35 40 45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr Ser

55 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu 85 90 . 95 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu Ser Asp Ile Phe Arg Ala Val Pro Phe Ile Ser Asp Val Phe Gln Gln Val Glu His Ile Ser Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp Thr Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr 165 170 175 Pro Cys Thr Thr Ser Met Ser Asn Glu Val Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser 200 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Arg 225 230 235 230 Pro Asn Cys Leu Ser Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Asn Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala 280 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Val Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr 330 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr Ala Thr Thr Thr Thr Ala Phe Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu 375 Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala

Gln	Lys	Leu	Lys		Asn	Val	Ser	Gly	Ser 410	Thr	His	Leu	Cys	Leu 415	Ser
Asp	Ser	Asp	Phe 420	Gly	Lys	Asp	Gly	Leu 425	Ala	Gly	Ala	Ser	Ser 430	His	Ile
Thr	Thr		Ser		Ala	Ala	Pro 440	Pro	Ser	Cys	Ser	Leu 445	Ser	Ser	Leu
Pro	Val 450	Leu	Met	Leu		Ala 455		Ala	Ala	Leu	Leu 460	Ser	Val	Ser	Leu

Ala Glu Thr Ser 465

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature (B) LOCATION: 1..539
- (D) OTHER INFORMATION: /note= "1 to 539 is -237 to 301 of Figure 5 Gdnfr"
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 540..1937
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA ACATCCCTAA	60
CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG GCCCAACTCG GCCCTTCGAG	120
CTCTCGAAGA TTACCGCATC TATTTTTTT TTCTTTTTTT TCTTTTCCTA GCGCAGATAA	180
AGTGAGCCCG GAAAGGGAAG GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG	240
TAAATAAACA AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT	300
CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG AGCTGAGTCG	360
CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT TCACTGGATG GAGCTGAACT	420
TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG GGATCGCTGC ACGCTGAGCT CCCTCGGCAA	480
GACCCAGCGG CGGCTCGGGA TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACC	539
ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu 1 5 10 15	587
CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala	635

	20	25		30	
AGT GAT CAG T Ser Asp Gln C 35	CGC CTG AAG Cys Leu Lys	GAG CAG AGC Glu Gln Ser 40	TGC AGC A	ACC AAG TAC (Thr Lys Tyr A 45	CGC ACG 683 Arg Thr
CTA AGG CAG T Leu Arg Gln C 50	GC GTG GCG Cys Val Ala	GGC AAG GAG Gly Lys Glu 55	ACC AAC T Thr Asn E	TTC AGC CTG (Phe Ser Leu <i>P</i> 60	GCA TCC 731 Ala Ser
GGC CTG GAG G Gly Leu Glu A 65	GCC AAG GAT Ala Lys Asp 70	GAG TGC CGC Glu Cys Arg	AGC GCC A Ser Ala M 75	ATG GAG GCC (Met Glu Ala I	CTG AAG 779 Leu Lys 80
CAG AAG TCG C Gln Lys Ser L	CTC TAC AAC Leu Tyr Asn 85	TGC CGC TGC Cys Arg Cys	AAG CGG C Lys Arg C 90	GGT ATG AAG A Gly Met Lys I	AAG GAG 827 Lys Glu 95
AAG AAC TGC C Lys Asn Cys L 1	CTG CGC ATT Leu Arg Ile 100	TAC TGG AGC Tyr Trp Ser 105	Met Tyr G	CAG AGC CTG (Gln Ser Leu (110	CAG GGA 875 Gln Gly
AAT GAT CTG C Asn Asp Leu L 115	CTG GAG GAT Leu Glu Asp	TCC CCA TAT Ser Pro Tyr 120	GAA CCA G	GTT AAC AGC A Val Asn Ser A 125	AGA TTG 923 Arg Leu
TCA GAT ATA T Ser Asp Ile F 130	TTC CGG GTG Phe Arg Val	GTC CCA TTC Val Pro Phe 135	: Ile Ser A	GAT GTT TTT (Asp Val Phe (140	CAG CAA 971 Gln Gln
GTG GAG CAC A Val Glu His I 145	ATT CCC AAA lle Pro Lys 150	GGG AAC AAC Gly Asn Asn	TGC CTG C Cys Leu A 155	GAT GCA GCG A Asp Ala Ala I	AAG GCC 1019 Lys Ala 160
TGC AAC CTC G Cys Asn Leu A	GAC GAC ATT Asp Asp Ile 165	TGC AAG AAG Cys Lys Lys	TAC AGG T Tyr Arg S 170	Ser Ala Tyr 1	ATC ACC 1067 Ile Thr 175
CCG TGC ACC A Pro Cys Thr T	ACC AGC GTG Thr Ser Val	TCC AAN GAT Ser Xaa Asp 185	Val Cys <i>F</i>	AAC CGC CGC A Asn Arg Arg I 190	AAG TGC 1115 Lys Cys
CAC AAG GCC C His Lys Ala I 195	CTC CGG CAG Leu Arg Gln	TTC TTT GAC Phe Phe Asp 200	AAG GTC C Lys Val I	CCG GCC AAG C Pro Ala Lys F 205	CAC AGC 1163 His Ser
TAC GGA ATG C Tyr Gly Met I 210	CTC TTC TGC Leu Phe Cys	TCC TGC CGG Ser Cys Arg 215	Asp Ile A	GCC TGC ACA (Ala Cys Thr (220	GAG CGG 1211 Glu Arg
AGG CGA CAG A Arg Arg Gln T 225	ACC ATC GTG Thr Ile Val 230	CCT GTG TGC Pro Val Cys	Ser Tyr C 235	GAA GAG AGG (Glu Glu Arg (GAG AAG 1259 Glu Lys 240
CCC AAC TGT T Pro Asn Cys I	TTG AAT TTG Leu Asn Leu 245	CAG GAC TCC Gln Asp Ser	TGC AAG A Cys Lys 1 250	Thr Asn Tyr	ATC TGC 1307 Ile Cys 255
AGA TCT CGC C Arg Ser Arg I	CTT GCG GAT Leu Ala Asp 260	TTT TTT ACC Phe Phe Thr 265	Asn Cys (CAG CCA GAG S Gln Pro Glu S 270	TCA AGG 1355 Ser Arg
TCT GTC AGC A Ser Val Ser S	AGC TGT CTA Ser Cys Leu	AAG GAA AAC Lys Glu Asn	TAC GCT (Tyr Ala A	GAC TGC CTC (Asp Cys Leu l	CTC GCC 1403 Leu Ala

275	280		285	
TAC TCG GGG CTT ATT Tyr Ser Gly Leu Ile 290	GGC ACA GTC AT Gly Thr Val Me 295	G ACC CCC AAC et Thr Pro Asn 300	TAC ATA GAC TCC Tyr Ile Asp Ser	1451
AGT AGC CTC AGT GTG Ser Ser Leu Ser Val 305	GCC CCA TGG TG Ala Pro Trp Cy 310	GT GAC TGC AGC vs Asp Cys Ser 315	AAC AGT GGG AAC Asn Ser Gly Asn 320	1499
GAC CTA GAA GAG TGC Asp Leu Glu Glu Cys 325	TTG AAA TTT TT Leu Lys Phe Le	rG AAT TTC TTC eu Asn Phe Phe 330	AAG GAC AAT ACA Lys Asp Asn Thr 335	1547
TGT CTT AAA AAT GCA Cys Leu Lys Asn Ala 340	ATT CAA GCC TT Ile Gln Ala Ph 34	e Gly Asn Gly	TCC GAT GTG ACC Ser Asp Val Thr 350	1595
GTG TGG CAG CCA GCC Val Trp Gln Pro Ala 355	TTC CCA GTA CA Phe Pro Val G1 360	G ACC ACC ACT n Thr Thr Thr	GCC ACT ACC ACC Ala Thr Thr Thr 365	1643
ACT GCC CTC CGG GTT Thr Ala Leu Arg Val 370	AAG AAC AAG CC Lys Asn Lys Pr 375	C CTG GGG CCA to Leu Gly Pro 380	GCA GGG TCT GAG Ala Gly Ser Glu	1691
AAT GAA ATT CCC ACT Asn Glu Ile Pro Thr 385	CAT GTT TTG CC His Val Leu Pr 390	CA CCG TGT GCA TO Pro Cys Ala 395	AAT TTA CAG GCA Asn Leu Gln Ala 400	1739
CAG AAG CTG AAA TCC Gln Lys Leu Lys Ser 405	AAT GTG TCG GG Asn Val Ser Gl	GC AAT ACA CAC Y Asn Thr His 410	CTC TGT ATT TCC Leu Cys Ile Ser 415	1787
AAT GGT AAT TAT GAA Asn Gly Asn Tyr Glu 420	AAA GAA GGT CT Lys Glu Gly Le 42	eu Gly Ala Ser	AGC CAC ATA ACC Ser His Ile Thr 430	1835
ACA AAA TCA ATG GCT Thr Lys Ser Met Ala 435	GCT CCT CCA AG Ala Pro Pro Se 440	C TGT GGT CTG r Cys Gly Leu	AGC CCA CTG CTG Ser Pro Leu Leu 445	1883
GTC CTG GTG GTA ACC Val Leu Val Val Thr 450	GCT CTG TCC AC Ala Leu Ser Th 455	C CTA TTA TCT r Leu Leu Ser 460	TTA ACA GAA ACA Leu Thr Glu Thr	1931
TCA TAG CTGCATTAAA 2 Ser * 465	AAAATACAAT ATGG	ACATGT AAAAAGA	ACAA AAACCAAGTT	1987
ATCTGTTTCC TGTTCTCT	TG TATAGCTGAA A	TTCCAGTTT AGGA	AGCTCAG TTGAGAAACA	2047
GTTCCATTCA ACTGGAAC	АТ ТТТТТТТТТ И	CCTTTTAAG AAAG	GCTTCTT GTGATCCTTC	2107
GGGGCTTCTG TGAAAAAC	CT GATGCAGTGC T	CCATCCAAA CTCA	AGAAGGC TTTGGGATAT	2167
GCTGTATTTT AAAGGGAC	AG TTTGTAACTT G	GGCTGTAAA GCAA	AACTGGG GCTGTGTTTT	2227
CGATGATGAT GATCATCA	TG ATCATGATNN N	ANNA NANANANAN	NUNUNUNUN NUNUNUNUN	2287
NNNNNNGAT TTTAACAG	TT TTACTTCTGG C	CTTTCCTAG CTAG	SAGAAGG AGTTAATATT	2347
TCTAAGGTAA CTCCCATA	TC TCCTTTAATG A	CATTGATTT CTAA	ATGATAT AAATTTCAGC	2407

GCCAAGCTTT	TTTGCCACAA	AGAAGATTCT	TACCAAGAGT	GGGCTTTGTG	2467
GTACTGATGT	TCACCTTTAT	ATATGTACTA	GCATTTTCCA	CGCTGATGTT	2527
AAACAGTTCT	GCACTCTTGT	ACAAAAGAAA	AAACACCTGT	CACATCCAAA	2587
GTCTTTTCGT	CAAAATAGAG	AGTGGGGAAT	GAGTGTGCCG	ATTCAATACC	2647
AACGACACTC	TCCTAATCCT	AAGCCTTACC	TGAGTGAGAA	GCCCTTTACC	2707
CCAATATAGC	TGAAATGTCG	CTCTAATACT	CTTTACACAT	ATGAGGTTAT	2767
АААТТТТАСТ	ACTAAATGAT	TTCAACTATT	GGCTTTCTAT	ATTTTGAAAG	2827
GTCTCATTTT	TTTACTGATG	GTTTAATACA	AAATACACAG	AGCTTGTTTC	2887
TAGTGTTCGC	TCTGATATGA	ACTTCACAAA	TACAGCTCAT	CAAAAGCAGA	2947
CCTCGTGCTG	TAGCAGAAAG	TTCTGCATCA	TGTGACTGTG	GACAGGCAGG	3007
ACAGACAAGC	ATTGTCTTTT	GTCATTGCTC	GAAGTGCAAG	CGTGCATACC	3067
ACTGGTGGCT	GCTTGTAAAT	GTTCTGCAGC	ATCTCTTGAC	ACACTTGTCA	3127
CAGTACCTTG	GTTTTCAGGT	TATCTGACAA	AGGCAGCTTT	GATTGGGACA	3187
GGCAGGCCGG	AA				3209
	GTACTGATGT AAACAGTTCT GTCTTTTCGT AACGACACTC CCAATATAGC AAATTTTACT GTCTCATTTT TAGTGTTCGC CCTCGTGCTG ACAGACAAGC ACTGGTGGCT CAGTACCTTG	GTACTGATGT TCACCTTTAT AAACAGTTCT GCACACTTGT GTCTTTTCGT CAAAATAGAG AACGACACTC TCCTAATCCT CCAATATAGC TGAAATGAT AAATTTTACT ACTAAATGAT GTCTCATTTT TTTACTGATG TAGTGTTCGC TCTGATATGA CCTCGTGCTG TAGCAGAAAG ACAGACAAGC ATTGTCTTTT ACTGGTGGCT GCTTGTAAAT	GTACTGATGT TCACCTTTAT ATATGTACTA AAACAGTTCT GCACTCTTGT ACAAAAGAAA GTCTTTTCGT CAAAATAGAG AGTGGGGAAT AACGACACTC TCCTAATCCT AAGCCTTACC CCAATATAGC TGAAAATGTCG CTCTAATACT AAATTTTACT ACTAAATGAT TTCAACTATT GTCTCATTTT TTTACTGATG GTTTAATACA TAGTGTCGC TAGCAGAAAG TTCTGCATCA ACAGACAAGC ATTGTCTTTT GTCATTGCTC ACTGGTGGCT GCTTGTAAAT GTTCTGCAGC CAGTACCTTG GTTTTCAGGT TATCTGACAA	GTACTGATGTTCACCTTTATATATGTACTAGCATTTCCAAAACAGTTCTGCACTCTTGTACAAAAGAAAAAACACCTGTGTCTTTTCGTCAAAATAGAGAGTGGGGAATGAGTGTGCCGAACGACACTCTCCTAATCCTAAGCCTTACCTGAGTGAGAACCAATATAGCTGAAAATGACCTCTAATACTCTTTACACATAAATTTTACTACTAAATGATTTCAACTATTGGCTTTCTATGTCTCATTTTTTTACTGATGGTTTAATACAAAATACACAGTAGTGTTCGCTCTGATATGAACTTCACAAATACAGCTCATACAGACAAGCATTGTCTTTTGTCATTGCTCGAAGTGCAAGACTGGTGGCTGCTTGTAAATGTTCTGACAAATCTCTTGACCAGTACCTTGGTTTTCAGGTTATCTGACAAAGGCAGCTTT	GCCAAGCTTT TTTGCCACAA AGAAGATTCT TACCAAGAGT GGGCTTTGTG GTACTGATGT TCACCTTTAT ATATGTACTA GCATTTTCCA CGCTGATGTT AAACAGTTCT GCACTCTTGT ACAAAAGAAA AAACACCTGT CACATCCAAA GTCTTTTCGT CAAAATAGAG AGTGGGGAAT GAGTGTGCCG ATTCAATACC AACGACACTC TCCTAATCCT AAGCCTTACC TGAGTGAGAA GCCCTTTACC CCAATATAGC TGAAATGAC CTCTAATACT CTTTACACAT ATGAGGTTAT AAATTTTACT ACTAAATGAT TTCAACTATT GGCTTTCTAT ATTTTGAAAG GTCTCATTTT TTTACTGATG GTTTAATACA AAATACACAG AGCTTGTTC TAGTGTTCGC TCTGATATGA ACTTCACAAA TACAGCTCAT CAAAAGCAGA CCTCGTGCTG TAGCAGAAAG TTCTGCATCA TGTGACTGT GACAGGCAGG ACAGACAAGC ATTGTCTTTT GTCATTGCACA ATCTCTTGAC ACACTTGTCA CAGTACCTTG GCTTGTAAAT GTTCTGCACA AGGCAGCTTT GATTGGACA GGCAGGCCGG AA

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 466 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr 170 165 Pro Cys Thr Thr Ser Val Ser Xaa Asp Val Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser 200 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg 215 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg 260 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala 280 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr 330 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu 375 Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala 385 390 395 400 390 Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu 440 Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr

Ser *

	_	_
~	-	•

(2)	INFORMATION	FOR	SEO	ID	NO:7:
-----	-------------	-----	-----	----	-------

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 base pairs

 - (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..508
 (D) OTHER INFORMATION: /note= "1 to 508 is -237 to 272 of Figure 5 Hsgr-21af"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTGGCCTCG GAACACGCCA	TTCTCCGCGC	CGCTTCCAAT	AACCACTAAC	ATCCCTAACG	60
AGCATCCGAG CCGAGGGCTC	TGCTCGGAAA	TCGTCCTGGC	CCAACTCGGC	CCTTCGAGCT	120
CTCGAAGATT ACCGCATCTA	TTTTTTTTT	CTTTTTTTC	TTTTCCTAGC	GCAGATAAAG	180
TGAGCCCGGA AAGGGAAGGA	GGGGGCGGG	ACACCATTGC	CCTGAAAGAA	TAAATAAGTA	240
AATAAACAAA CTGGCTCCTC	GCCGCAGCTG	GACGCGGTCG	GTTGAGTCCA	GGTTGGGTCG	300
GACCTGAACC CCTAAAAGCG	GAACCGCCTC	CCGCCCTCGC	CATCCCGGAG	CTGAGTCGCC	360
GGCGGCGGTG GCTGCTGCCA	GACCCGGAGT	TTCCTCTTTC	ACTGGATGGA	GCTGAACTTT	420
GGGCGGCCAG AGCAGCACAG	CTGTCCGGGG	ATCGCTGCAC	GCTGAGCTCC	CTCGGCAAGA	480
CCCAGCGGCG GCTCGGGATT	TTTTTGGG				508

- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 510 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..510
 - (D) OTHER INFORMATION: /note= "1 to 510 is -237 to 272 of Figure 5 Hsgr-21bf"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
- AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA ACATCCCTAA 60 CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG GCCCAACTCG GCCCTTCGAG 120

CTCTCGAAGA	TTACCGCATC	${\bf TATTTTTTT}$	TTCTTTTTT	TCTTTTCCTA	GCGCAGATAA	180
AGTGAGCCCG	GAAAGGGAAG	GAGGGGGCGG	GGACACCATT	GCCCTGAAAG	AATAAATAAG	240
ТАААТАААСА	AACTGGCTCC	TCGCCGCAGC	TGGACGCGGT	CGGTTGAGTC	CAGGTTGGGT	300
CGGACCTGAA	CCCCTAAAAG	CGGAACCGCC	TCCCGCCCTC	GCCATCCCGG	AGCTGAGTCG	360
ccgccgccg	TGGCTGCTGC	CAGACCCGGA	GTTTCCTCTT	TCACTGGATG	GAGCTGAACT	420
TTGGGCGGCC	AGAGCAGCAC	AGCTGTCCGG	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCAA	480
GACCCAGCGG	CGGCTCGGGA	TTTTTTTGGG				510

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1927 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 538..1926
- (ix) FEATURE:
- (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..537
 (D) OTHER INFORMATION: /note= "1 to 537 is -235 to 301 of Figure 5 21acon"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCTGGCCTCG GAACACGCCA TTCTCCGCGC CGCTTCCAAT AACCACTAAC ATCCCTAACG	60
AGCATCCGAG CCGAGGGCTC TGCTCGGAAA TCGTCCTGGC CCAACTCGGC CCTTCGAGCT	120
CTCGAAGATT ACCGCATCTA TTTTTTTTT CTTTTTTTC TTTTCCTAGC GCAGATAAAG	180
TGAGCCCGGA AAGGGAAGGA GGGGGCGGGG ACACCATTGC CCTGAAAGAA TAAATAAGTA	240
AATAAACAAA CTGGCTCCTC GCCGCAGCTG GACGCGGTCG GTTGAGTCCA GGTTGGGTCG	300
GACCTGAACC CCTAAAAGCG GAACCGCCTC CCGCCCTCGC CATCCCGGAG CTGAGTCGCC	360
GGCGGCGGTG GCTGCTGCCA GACCCGGAGT TTCCTCTTTC ACTGGATGGA GCTGAACTTT	420
GGGCGGCCAG AGCAGCACAG CTGTCCGGGG ATCGCTGCAC GCTGAGCTCC CTCGGCAAGA	480
CCCAGCGGCG GCTCGGGATT TTTTTGGGGG GGCGGGGACC AGCCCCGCGC CGGCACC	537
ATG TTC CTG GCG NCC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC Met Phe Leu Ala Xaa Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu 1 5	585
CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala 20 25 30	633

AGT Ser	GAT Asp	CAG Gln 35	TGC Cys	CTG Leu	AAG Lys	GAG Glu	CAG Gln 40	AGC Ser	TGC Cys	AGC Ser	ACC Thr	AAG Lys 45	TAC Tyr	CGC Arg	ACG Thr	681
CTA Leu	AGG Arg 50	CAG Gln	TGC Cys	GTG Val	GCG Ala	GGC Gly 55	AAG Lys	GAG Glu	ACC Thr	AAC Asn	TTC Phe 60	AGC Ser	CTG Leu	GCA Ala	TCC Ser	729
GGC Gly 65	CTG Leu	GAG Glu	GCC Ala	AAG Lys	GAT Asp 70	GAG Glu	TGC Cys	CGC Arg	AGC Ser	GCC Ala 75	ATG Met	GAG Glu	GCC Ala	CTG Leu	AAG Lys 80	777
CAG Gln	AAG Lys	TCG Ser	CTC Leu	TAC Tyr 85	AAC Asn	TGC Cys	CGC Arg	TGC Cys	AAG Lys 90	CGG Arg	GGT Gly	ATG Met	AAG Lys	AAG Lys 95	GAG Glu	825
AAG Lys	AAC Asn	TGC Cys	CTG Leu 100	CGC Arg	ATT Ile	TAC Tyr	TGG Trp	AGC Ser 105	ATG Met	TAC Tyr	CAG Gln	AGC Ser	CTG Leu 110	CAG Gln	GGA Gly	873
AAT Asn	GAT Asp	CTG Leu 115	CTG Leu	GAG Glu	GAT Asp	TCC Ser	CCA Pro 120	TAT Tyr	GAA Glu	CCA Pro	GTT Val	AAC Asn 125	AGC Ser	AGA Arg	TTG Leu	921
TCA Ser	GAT Asp 130	ATA Ile	TTC Phe	CGG Arg	GTG Val	GTC Val 135	CCA Pro	TTC Phe	ATA Ile	TCA Ser	GAT Asp 140	GTT Val	TTT Phe	CAG Gln	CAA Gln	969
GTG Val 145	GAG Glu	CAC His	ATT Ile	CCC Pro	AAA Lys 150	GGG Gly	AAC Asn	AAC Asn	TGC Cys	CTG Leu 155	GAT Asp	GCA Ala	GCG Ala	AAG Lys	GCC Ala 160	1017
TGC Cys	AAC Asn	CTC Leu	GAC Asp	GAC Asp 165	ATT Ile	TGC Cys	AAG Lys	AAG Lys	TAC Tyr 170	AGG Arg	TCG Ser	GCG Ala	TAC Tyr	ATC Ile 175	ACC Thr	1065
CCG Pro	TGC Cys	ACC Thr	ACC Thr 180	AGC Ser	GTG Val	TCC Ser	AAC Asn	GAT Asp 185	GTC Val	TGC Cys	AAC Asn	CGC Arg	CGC Arg 190	AAG Lys	TGC Cys	1113
CAC His	AAG Lys	GCC Ala 195	CTC Leu	CGG Arg	CAG Gln	TTC Phe	TTT Phe 200	GAC Asp	AAG Lys	GTC Val	CCG Pro	GCC Ala 205	AAG Lys	CAC His	AGC Ser	1161
TAC Tyr	GGA Gly 210	ATG Met	CTC Leu	TTC Phe	TGC Cys	TCC Ser 215	TGC Cys	CGG Arg	GAC Asp	ATC Ile	GCC Ala 220	TGC Cys	ACA Thr	GAG Glu	CGG Arg	1209
AGG Arg 225	CGA Arg	CAG Gln	ACC Thr	ATC Ile	GTG Val 230	CCT Pro	GTG Val	TGC Cys	TCC Ser	TAT Tyr 235	GAA Glu	GAG Glu	AGG Arg	GAG Glu	AAG Lys 240	1257
CCC Pro	AAC Asn	TGT Cys	TTG Leu	AAT Asn 245	TTG Leu	CAG Gln	GAC Asp	TCC Ser	TGC Cys 250	AAG Lys	ACG Thr	AAT Asn	TAC Tyr	ATC Ile 255	TGC Cys	1305
AGA Arg	TCT Ser	CGC Arg	CTT Leu 260	GCG Ala	GAT Asp	TTT Phe	TTT Phe	ACC Thr 265	AAC Asn	TGC Cys	CAG Gln	CCA Pro	GAG Glu 270	TCA Ser	AGG Arg	1353
TCT Ser	GTC Val	AGC Ser 275	AGC Ser	TGT Cys	CTA Leu	AAG Lys	GAA Glu 280	AAC Asn	TAC Tyr	GCT Ala	GAC Asp	TGC Cys 285	CTC Leu	CTC Leu	GCC Ala	1401

TAC Tyr	TCG Ser 290	GGG Gly	CTT Leu	ATT Ile	GGC Gly	ACA Thr 295	GTC Val	ATG Met	ACC Thr	CCC Pro	AAC Asn 300	TAC Tyr	ATA Ile	GAC Asp	TCC Ser	1449
AGT Ser 305	AGC Ser	CTC Leu	AGT Ser	GTG Val	GCC Ala 310	CCA Pro	TGG Trp	TGT Cys	GAC Asp	TGC Cys 315	AGC Ser	AAC Asn	AGT Ser	GGG Gly	AAC Asn 320	1497
GAC Asp	CTA Leu	GAA Glu	GAG Glu	TGC Cys 325	TTG Leu	AAA Lys	TTT Phe	TTG Leu	AAT Asn 330	TTC Phe	TTC Phe	AAG Lys	GAC Asp	AAT Asn 335	ACA Thr	1545
TGT Cys	CTT Leu	AAA Lys	AAT Asn 340	GCA Ala	ATT Ile	CAA Gln	GCC Ala	TTT Phe 345	GGC Gly	AAT Asn	GGC Gly	TCC Ser	GAT Asp 350	GTG Val	ACC Thr	1593
GTG Val	TGG Trp	CAG Gln 355	CCA Pro	GCC Ala	TTC Phe	CCA Pro	GTA Val 360	CAG Gln	ACC Thr	ACC Thr	ACT Thr	GCC Ala 365	ACT Thr	ACC Thr	ACC Thr	1641
ACT Thr	GCC Ala 370	CTC Leu	CGG Arg	GTT Val	AAG Lys	AAC Asn 375	AAG Lys	CCC Pro	CTG Leu	GGG Gly	CCA Pro 380	GCA Ala	GGG Gly	TCT Ser	GAG Glu	1689
AAT Asn 385	GAA Glu	ATT Ile	CCC Pro	ACT Thr	CAT His 390	GTT Val	TTG Leu	CCA Pro	CCG Pro	TGT Cys 395	GCA Ala	AAT Asn	TTA Leu	CAG Gln	GCA Ala 400	1737
CAG Gln	AAG Lys	CTG Leu	AAA Lys	TCC Ser 405	AAT Asn	GTG Val	TCG Ser	GGC Gly	AAT Asn 410	ACA Thr	CAC His	CTC Leu	TGT Cys	ATT Ile 415	TCC Ser	1785
AAT Asn	GGT Gly	AAT Asn	TAT Tyr 420	GAA Glu	AAA Lys	GAA Glu	GGT Gly	CTC Leu 425	GGT Gly	GCT Ala	TCC Ser	AGC Ser	CAC His 430	ATA Ile	ACC Thr	1833
ACA Thr	AAA Lys	TCA Ser 435	ATG Met	GCT Ala	GCT Ala	CCT Pro	CCA Pro 440	AGC Ser	TGT Cys	GGT Gly	CTG Leu	AGC Ser 445	CCA Pro	CTG Leu	CTG Leu	1881
GTC Val	CTG Leu 450	GTG Val	GTA Val	ACC Thr	GCT Ala	CTG Leu 455	TCC Ser	ACC Thr	CTA Leu	TTA Leu	TCT Ser 460	TTA Leu	ACA Thr	GAA Glu		1926
A																1927

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Phe Leu Ala Xaa Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu 1 5 10 15

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala 20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser 50 55 60 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
70 75 80 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu 120 Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr 165 Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser 200 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg 215 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys 225 230 235 240 Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala 280 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr 330 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu

	370					375					380						
Asn 385	Glu	Ile	Pro	Thr	His 390	Val	Leu	Pro	Pro	Cys 395	Ala	Asn	Leu	Gln	Ala 400		
Gln	Lys	Leu	Lys	Ser 405	Asn	Val	Ser	Gly	Asn 410	Thr	His	Leu	Cys	Ile 415	Ser		
Asn	Gly	Asn	Tyr 420	Glu	Lys	Glu	Gly	Leu 425	Gly	Ala	Ser	Ser	His 430	Ile	Thr		
Thr	Lys	Ser 435	Met	Ala	Ala	Pro	Pro 440	Ser	Cys	Gly	Leu	Ser 445	Pro	Leu	Leu		
Val	Leu 450	Val	Val	Thr	Ala	Leu 455	Ser	Thr	Leu	Leu	Ser 460	Leu	Thr	Glu			
(2)	INFO	ORMA!	rion	FOR	SEQ	ID I	10:11	L:									
F:	(ii) (ix) (ix)	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	A) Li B) T C) S C) S C) T C ATURI ATURI A) N B) L C ATURI C) O C C C) O C C C C C C C C C C C C C C C C C C C	ENGTHYPE: PRANIOPOLO LE TY E: AME/I OCATY CHER OCATY	HARACHE 19 INTO DEDNI DGY: YPE: KEY: ION: INFO	CDS 540 misc	case acid single a	pain l gle 28 ature :/no	e ote=			39 is	s -23	37 to	o 301	of	
AAT												ACCA	CTA A	ACATO	CCTA	A	60
															rtcga		120
CTC	rcga/	AGA :	TTAC	CGCA	rc T	ATTT:	rTTT	י דד	CTTT	rttt	TCTT	TTTC	CTA (GCGC2	AGATA	A	180
AGT	GAGC	CCG (GAAA	GGGA	AG GA	AGGG	GCG	G GG	ACAC	CATT	GCC	CTGA	AAG A	ATA	AATAA	З	240
TAA	AAATA	ACA A	AACT	GGCT	CC TO	CGCC	GCAG	C TGC	GACGO	CGGT	CGG	TGAC	TC (CAGG	rtggg'	r	300
CGG	ACCTO	GAA (cccc'	ГААА	AG CO	GGAA	CCGC	C TCC	CCGC	CCTC	GCCZ	ATCC	CGG Z	AGCT	GAGTC	3	360
CCG	GCGG	CGG (rggc	rgc T	GC C	AGAC	CCGGZ	A GT	rTCC:	гстт	TCAC	CTGG	ATG (GAGC	rgaac'	г	420
TTG	GCG	GCC Z	AGAG	CAGC	AC AC	GCTG	rccgo	G GGZ	ATCG	CTGC	ACG	CTGA	GCT (CCT	CGGCA	A	480
GAC	CCAG	CGG (CGGC'	rcgg	GA T	r TTT T	rtgg	G GG	GCG	GGGA	CCA	CCC	CGC (GCCG	GCACC		539
ATG Met 1	TTC Phe	CTG Leu	GCG Ala	ACC Thr 5	CTG Leu	TAC Tyr	TTC Phe	GCG Ala	CTG Leu 10	CCG Pro	CTC Leu	TTG Leu	GAC Asp	TTG Leu 15	CTC Leu		587

CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC 635

Leu	Ser	Ala	Glu 20	Val	Ser	Gly	Gly	Asp 25	Arg	Leu	Asp	Cys	Val 30	Lys	Ala	
AGT Ser	GAT Asp	CAG Gln 35	TGC Cys	CTG Leu	AAG Lys	GAG Glu	CAG Gln 40	AGC Ser	TGC Cys	AGC Ser	ACC Thr	AAG Lys 45	TAC Tyr	CGC Arg	ACG Thr	683
CTA Leu	AGG Arg 50	CAG Gln	TGC Cys	GTG Val	GCG Ala	GGC Gly 55	AAG Lys	GAG Glu	ACC Thr	AAC Asn	TTC Phe 60	AGC Ser	CTG Leu	GCA Ala	TCC Ser	731
GGC Gly 65	CTG Leu	GAG Glu	GCC Ala	AAG Lys	GAT Asp 70	GAG Glu	TGC Cys	CGC Arg	AGC Ser	GCC Ala 75	ATG Met	GAG Glu	GCC Ala	CTG Leu	AAG Lys 80	779
CAG Gln	AAG Lys	TCG Ser	CTC Leu	TAC Tyr 85	AAC Asn	TGC Cys	CGC Arg	TGC Cys	AAG Lys 90	CGG Arg	GGT Gly	ATG Met	AAG Lys	AAG Lys 95	GAG Glu	827
AAG Lys	AAC Asn	TGC Cys	CTG Leu 100	CGC Arg	ATT Ile	TAC Tyr	TGG Trp	AGC Ser 105	ATG Met	TAC Tyr	CAG Gln	AGC Ser	CTG Leu 110	CAG Gln	GGA Gly	875
AAT Asn	GAT Asp	CTG Leu 115	CTG Leu	GAG Glu	GAT Asp	TCC Ser	CCA Pro 120	TAT Tyr	GAA Glu	CCA Pro	GTT Val	AAC Asn 125	AGC Ser	AGA Arg	TTG Leu	923
TCA Ser	GAT Asp 130	ATA Ile	TTC Phe	CGG Arg	GTG Val	GTC Val 135	CCA Pro	TTC Phe	ATA Ile	TCA Ser	GAT Asp 140	GTT Val	TTT Phe	CAG Gln	CAA Gln	971
GTG Val 145	GAG Glu	CAC His	ATT Ile	CCC Pro	AAA Lys 150	GGG Gly	AAC Asn	AAC Asn	TGC Cys	CTG Leu 155	GAT Asp	GCA Ala	GCG Ala	AAG Lys	GCC Ala 160	1019
TGC Cys	AAC Asn	CTC Leu	GAC Asp	GAC Asp 165	ATT Ile	TGC Cys	AAG Lys	AAG Lys	TAC Tyr 170	AGG Arg	TCG Ser	GCG Ala	TAC Tyr	ATC Ile 175	ACC Thr	1067
CCG Pro	TGC Cys	ACC Thr	ACC Thr 180	AGC Ser	GTG Val	TCC Ser	AAC Asn	GAT Asp 185	GTC Val	TGC Cys	AAC Asn	CGC Arg	CGC Arg 190	AAG Lys	TGC Cys	1115
CAC His	AAG Lys	GCC Ala 195	CTC Leu	CGG Arg	CAG Gln	TTC Phe	TTT Phe 200	GAC Asp	AAG Lys	GTC Val	CCG Pro	GCC Ala 205	AAG Lys	CAC His	AGC Ser	1163
TAC Tyr	GGA Gly 210	ATG Met	CTC Leu	TTC Phe	TGC Cys	TCC Ser 215	TGC Cys	CGG Arg	GAC Asp	ATC Ile	GCC Ala 220	TGC Cys	ACA Thr	GAG Glu	CGG Arg	1211
AGG Arg 225	CGA Arg	CAG Gln	ACC Thr	ATC Ile	GTG Val 230	CCT Pro	GTG Val	TGC Cys	TCC Ser	TAT Tyr 235	GAA Glu	GAG Glu	AGG Arg	GAG Glu	AAG Lys 240	1259
CCC Pro	AAC Asn	TGT Cys	TTG Leu	AAT Asn 245	TTG Leu	CAG Gln	GAC Asp	TCC Ser	TGC Cys 250	AAG Lys	ACG Thr	AAT Asn	TAC Tyr	ATC Ile 255	TGC Cys	1307
AGA Arg	TCT Ser	CGC Arg	CTT Leu 260	GCG Ala	GAT Asp	TTT Phe	TTT Phe	ACC Thr 265	AAC Asn	TGC Cys	CAG Gln	CCA Pro	GAG Glu 270	TCA Ser	AGG Arg	1355
TCT	GTC	AGC	AGC	TGT	CTA	AAG	GAA	AAC	TAC	GCT	GAC	TGC	CTC	CTC	GCC	1403

Ser	Val	Ser 275	Ser	Cys	Leu	Lys	Glu 280	Asn	Tyr	Ala	Asp	Cys 285	Leu	Leu	Ala	
TAC Tyr	TCG Ser 290	GGG Gly	CTT Leu	ATT Ile	GGC Gly	ACA Thr 295	GTC Val	ATG Met	ACC Thr	CCC Pro	AAC Asn 300	TAC Tyr	ATA Ile	GAC Asp	TCC Ser	1451
AGT Ser 305	AGC Ser	CTC Leu	AGT Ser	GTG Val	GCC Ala 310	CCA Pro	TGG Trp	TGT Cys	GAC Asp	TGC Cys 315	AGC Ser	AAC Asn	AGT Ser	GGG Gly	AAC Asn 320	1499
GAC Asp	CTA Leu	GAA Glu	GAG Glu	TGC Cys 325	TTG Leu	AAA Lys	TTT Phe	TTG Leu	AAT Asn 330	TTC Phe	TTC Phe	AAG Lys	GAC Asp	AAT Asn 335	ACA Thr	1547
TGT Cys	CTT Leu	AAA Lys	AAT Asn 340	GCA Ala	ATT Ile	CAA Gln	GCC Ala	TTT Phe 345	GGC Gly	AAT Asn	GGC Gly	TCC Ser	GAT Asp 350	GTG Val	ACC Thr	1595
GTG Val	TGG Trp	CAG Gln 355	CCA Pro	GCC Ala	TTC Phe	CCA Pro	GTA Val 360	CAG Gln	ACC Thr	ACC Thr	ACT Thr	GCC Ala 365	ACT Thr	ACC Thr	ACC Thr	1643
ACT Thr	GCC Ala 370	CTC Leu	CGG Arg	GTT Val	AAG Lys	AAC Asn 375	AAG Lys	CCC Pro	CTG Leu	GGG Gly	CCA Pro 380	GCA Ala	GGG Gly	TCT Ser	GAG Glu	1691
AAT Asn 385	GAA Glu	ATT Ile	CCC Pro	ACT Thr	CAT His 390	GTT Val	TTG Leu	CCA Pro	CCG Pro	TGT Cys 395	GCA Ala	AAT Asn	TTA Leu	CAG Gln	GCA Ala 400	1739
CAG Gln	AAG Lys	CTG Leu	AAA Lys	TCC Ser 405	AAT Asn	GTG Val	TCG Ser	GGC Gly	AAT Asn 410	ACA Thr	CAC His	CTC Leu	TGT Cys	ATT Ile 415	TCC Ser	1787
AAT Asn	GGT Gly	AAT Asn	TAT Tyr 420	GAA Glu	AAA Lys	GAA Glu	GGT Gly	CTC Leu 425	GGT Gly	GCT Ala	TCC Ser	AGC Ser	CAC His 430	ATA Ile	ACC Thr	1835
ACA Thr	AAA Lys	TCA Ser 435	ATG Met	GCT Ala	GCT Ala	CCT Pro	CCA Pro 440	AGC Ser	TGT Cys	GGT Gly	CTG Leu	AGC Ser 445	CCA Pro	CTG Leu	CTG Leu	1883
GTC Val	CTG Leu 450	GTG Val	GTA Val	ACC Thr	GCT Ala	CTG Leu 455	TCC Ser	ACC Thr	CTA Leu	TTA Leu	TCT Ser 460	TTA Leu	ACA Thr	GAA Glu		1928
A																1929

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu 10 NVLATLYFALPLLNLL

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser 50 55 60 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu 85 90 95 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly. Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala 150 Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys 185 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg 215 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg 265 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala 280 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser 295 Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn 310 Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr 330 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr

		355					360					365					
Thr	Ala 370	Leu	Arg	Val	Lys	Asn 375	Lys	Pro	Leu	Gly	Pro 380	Ala	Gly	Ser	Glu		
Asn 385	Glu	Ile	Pro	Thr	His 390	Val	Leu	Pro	Pro	Cys 395	Ala	Asn	Leu	Gln	Ala 400		
Gln	.Lys	Leu	Lys	Ser 405	Asn	Val	Ser	Gly	Asn 410	Thr	His	Leu	Cys	Ile 415	Ser		
Asn	Gly	Asn	Tyr 420	Glu	Lys	Glu	Gly	Leu 425	Gly	Ala	Ser	Ser	His 430	Ile	Thr		
Thr	Lys	Ser 435	Met	Ala	Ala	Pro	Pro 440	Ser	Cys	Gly	Leu	Ser 445	Pro	Leu	Leu		
Val	Leu 450	Val	Val	Thr	Ala	Leu 455	Ser	Thr	Leu	Leu	Ser 460	Leu	Thr	Glu			
(2)	INF	ORMA'	rion	FOR	SEQ	ID N	10:13	3:									
	(ii) (ix) igure (ix)	(1 (1) (1) (1) (1) (1) (2) (1) (1) (1) (1) (1) (1) (1) (1) (1) (1	ATURIAN NA	ENGTH YPE: TRANIO POLO LE TY E: AME/I DCAT: THER -29a' E: AME/I DCAT:	H: 69 nuclocal nucloc	CDS 2	ase racio singear a c_fear 597 ON: S	pairs i gle ature : /no	e ote=	0:13	:				1512	of	
G To	CG GC er Al	CG Ti la Ti	AC A' yr I:	rc Ad le Tl	CC CC nr Pi 5	CG TO	GC AC	CC AC	ar Se	GC G er Va 10	rg ro al Se	cc Ai er Ai	AT GA	sp Va	rc al 15		46
TGC Cys	AAC Asn	CGC Arg	CGC Arg	AAG Lys 20	TGC Cys	CAC His	AAG Lys	GCC Ala	CTC Leu 25	CGG Arg	CAG Gln	TTC Phe	TTT Phe	GAC Asp 30	AAG Lys		94
GTC Val	CCG Pro	GCC Ala	AAG Lys 35	CAC His	AGC Ser	TAC Tyr	GGA Gly	ATG Met 40	CTC Leu	TTC Phe	TGC Cys	TCC Ser	TGC Cys 45	CGG Arg	GAC Asp		142
ATC Ile	GCC Ala	TGC Cys 50	ACA Thr	GAG Glu	CGG Arg	AGG Arg	CGA Arg 55	CAG Gln	ACC Thr	ATC Ile	GTG Val	CCT Pro 60	GTG Val	TGC Cys	TCC Ser		190
TAT Tyr	GAA Glu 65	GAG Glu	AGG Arg	GAG Glu	AAG Lys	CCC Pro 70	AAC Asn	TGT Cys	TTG Leu	AAT Asn	TTG Leu 75	CAG Gln	GAC Asp	TCC Ser	TGC Cys		238

AAG Lys 80	ACG Thr	AAT Asn	TAC Tyr	ATC Ile	TGC Cys 85	AGA Arg	TCT Ser	CGC Arg	CTT Leu	GCG Ala 90	GAT Asp	TTT Phe	TTT Phe	ACC Thr	AAC Asn 95	286
TGC Cys	CAG Gln	CCA Pro	GAG Glu	TCA Ser 100	AGG Arg	TCT Ser	GTC Val	AGC Ser	AGC Ser 105	TGT Cys	CTA Leu	AAG Lys	GAA Glu	AAC Asn 110	TAC Tyr	334
GCT Ala	GAC Asp	TGC Cys	CTC Leu 115	CTC Leu	GCC Ala	TAC Tyr	TCG Ser	GGG Gly 120	CTT Leu	ATT Ile	GGC Gly	ACA Thr	GTC Val 125	ATG Met	ACC Thr	382
CCC Pro	AAC Asn	TAC Tyr 130	ATA Ile	GAC Asp	TCC Ser	AGT Ser	AGC Ser 135	CTC Leu	AGT Ser	GTG Val	GCC Ala	CCA Pro 140	TGG Trp	TGT Cys	GAC Asp	430
TGC Cys	AGC Ser 145	AAC Asn	AGT Ser	GGG Gly	AAC Asn	GAC Asp 150	CTA Leu	GAA Glu	GAG Glu	TGC Cys	TTG Leu 155	AAA Lys	TTT Phe	TTG Leu	AAT Asn	478
TTC Phe 160	TTC Phe	AAG Lys	GAC Asp	AAT Asn	ACA Thr 165	TGT Cys	CTT Leu	AAA Lys	AAT Asn	GCA Ala 170	ATT Ile	CAA Gln	GCC Ala	TTT Phe	GGC Gly 175	526
AAT Asn	GGC Gly	TCC Ser	GAT Asp	GTG Val 180	ACC Thr	GTG Val	TGG Trp	CAG Gln	CCA Pro 185	GCC Ala	TTC Phe	CCA Pro	GTA Val	CAG Gln 190	ACC Thr	574
ACC Thr	ACT Thr	GCC Ala	GCT Ala 195	ACC Thr	ACC Thr	ACT Thr	GCC Ala	CTC Leu 200	CGG Arg	GTT Val	AAG Lys	AAC Asn	AAG Lys 205	CCC Pro	CTG Leu	622
GGG Gly	CCA Pro	GCA Ala 210	GGG Gly	TCT Ser	GAG Glu	AAT Asn	GAA Glu 215	ATT Ile	CCC Pro	ACT Thr	CAT His	GTT Val 220	TTG Leu	CCA Pro	CCG Pro	670
TGT Cys	GCA Ala 225	AAT Asn	TTA Leu	CAG Gln	GCA Ala	CAG Gln 230	AAG Lys	CTG Leu	AA							699

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys 1 5 10 15

Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val 20 25 30

Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile 35 40 45

Ala Cys Thr Glu Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr 50 55 60

Glu 65	Glu	Arg	Glu	Lys	Pro 70	Asn	Cys	Leu	Asn	Leu 75	Gln	Asp	Ser	Cys	Lys 80
Thr	Asn	Tyr	Ile	Cys 85	Arg	Ser	Arg	Leu	Ala 90	Asp	Phe	Phe	Thr	Asn 95	Cys
Gln	Pro	Glu	Ser 100	Arg	Ser	Val	Ser	Ser 105	Cys	Leu	Lys	Glu	Asn 110	Tyr	Ala
Asp	Cys	Leu 115	Leu	Ala	Tyr	Ser	Gly 120	Leu	Ile	Gly	Thr	Val 125	Met	Thr	Pro
Asn	Tyr 130	Ile	Asp	Ser	Ser	Ser 135	Leu	Ser	Val	Ala	Pro 140	Trp	Cys	Asp	Cys
Ser 145	Asn	Ser	Gly	Asn	Asp 150	Leu	Glu	Glu	Cys	Leu 155	Lys	Phe	Leu	Asn	Phe 160
Phe	Lys	Asp	Asn	Thr 165	Cys	Leu	Lys	Asn	Ala 170	Ile	Gln	Ala	Phe	Gly 175	Asn
Gly	Ser	Asp	Val 180	Thr	Val	Trp	Gln	Pro 185	Ala	Phe	Pro	Val	Gln 190	Thr	Thr
Thr	Ala	Ala 195	Thr	Thr	Thr	Ala	Leu 200	Arg	Val	Lys	Asn	Lys 205	Pro	Leu	Gly
Pro	Ala 210	Gly	Ser	Glu	Asn	Glu 215	Ile	Pro	Thr	His	Val 220	Leu	Pro	Pro	Суз
Ala	Asn	Leu	Gln	Ala	Gln	Lys	Leu								

- (2) INFORMATION FOR SEQ ID NO:15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2157 base pairs (B) TYPE: nucleic acid

230

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 2..886
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..2157
- (D) OTHER INFORMATION: /note= "1 to 2157 is 814 to 2971 of Figure 5 29brc"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
- G TCG GCG TAC ATC ACC CCG TGC ACC ACC AGC GTG TCC AAT GAT GTC Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val 1
- TGC AAC CGC CGC AAG TGC CAC AAG GCC CTC CGG CAG TTC TTT GAC AAG 94 Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys 25 20

46

GTC Val	CCG Pro	GCC Ala	AAG Lys 35	CAC His	AGC Ser	TAC Tyr	GGA Gly	ATG Met 40	CTC Leu	TTC Phe	TGC Cys	TCC Ser	TGC Cys 45	CGG Arg	GAC Asp	142
ATC Ile	GCC Ala	TGC Cys 50	ACA Thr	GAG Glu	CGG Arg	AGG Arg	CGA Arg 55	CAG Gln	ACC Thr	ATC Ile	GTG Val	CCT Pro 60	GTG Val	TGC Cys	TCC Ser	190
TAT Tyr	GAA Glu 65	GAG Glu	AGG Arg	GAG Glu	AAG Lys	CCC Pro 70	AAC Asn	TGT Cys	TTG Leu	AAT Asn	TTG Leu 75	CAG Gln	GAC Asp	TCC Ser	TGC Cys	238
AAG Lys 80	ACG Thr	AAT Asn	TAC Tyr	ATC Ile	TGC Cys 85	AGA Arg	TCT Ser	CGC Arg	CTT Leu	GCG Ala 90	GAT Asp	TTT Phe	TTT Phe	ACC Thr	AAC Asn 95	286
TGC Cys	CAG Gln	CCA Pro	GAG Glu	TCA Ser 100	AGG Arg	TCT Ser	GTC Val	AGC Ser	AGC Ser 105	TGT Cys	CTA Leu	AAG Lys	GAA Glu	AAC Asn 110	TAC Tyr	334
GCT Ala	GAC Asp	TGC Cys	CTC Leu 115	CTC Leu	GCC Ala	TAC Tyr	TCG Ser	GGG Gly 120	CTT Leu	ATT Ile	GGC Gly	ACA Thr	GTC Val 125	ATG Met	ACC Thr	382
CCC Pro	AAC Asn	TAC Tyr 130	ATA Ile	GAC Asp	TCC Ser	AGT Ser	AGC Ser 135	CTC Leu	AGT Ser	GTG Val	GCC Ala	CCA Pro 140	TGG Trp	TGT Cys	GAC Asp	430
TGC Cys	AGC Ser 145	AAC Asn	AGT Ser	GGG Gly	AAC Asn	GAC Asp 150	CTA Leu	GAA Glu	GAG Glu	TGC Cys	TTG Leu 155	AAA Lys	TTT Phe	TTG Leu	AAT Asn	478
TTC Phe 160	TTC Phe	AAG Lys	GAC Asp	AAT Asn	ACA Thr 165	TGT Cys	CTT Leu	AAA Lys	AAT Asn	GCA Ala 170	ATT Ile	CAA Gln	GCC Ala	TTT Phe	GGC Gly 175	526
AAT Asn	GGC Gly	TCC Ser	GAT Asp	GTG Val 180	ACC Thr	GTG Val	TGG Trp	CAG Gln	CCA Pro 185	GCC Ala	TTC Phe	CCA Pro	GTA Val	CAG Gln 190	ACC Thr	574
ACC Thr	ACT Thr	GCC Ala	GCT Ala 195	ACC Thr	ACC Thr	ACT Thr	GCC Ala	CTC Leu 200	CGG Arg	GTT Val	AAG Lys	AAC Asn	AAG Lys 205	CCC Pro	CTG Leu	622
GGG Gly	CCA Pro	GCA Ala 210	GGG Gly	TCT Ser	GAG Glu	AAT Asn	GAA Glu 215	ATT Ile	CCC Pro	ACT Thr	CAT His	GTT Val 220	TTG Leu	CCA Pro	CCG Pro	670
TGT Cys	GCA Ala 225	AAT Asn	TTA Leu	CAG Gln	GCA Ala	CAG Gln 230	AAG Lys	CTG Leu	AAA Lys	TCC Ser	AAT Asn 235	GTG Val	TCG Ser	GGC Gly	AAT Asn	718
ACA Thr 240	CAC His	CTC Leu	TGT Cys	ATT Ile	TCC Ser 245	AAT Asn	GGT Gly	AAT Asn	TAT Tyr	GAA Glu 250	AAA Lys	GAA Glu	GGT Gly	CTC Leu	GGT Gly 255	766
GCT Ala	TCC Ser	AGC Ser	CAC His	ATA Ile 260	ACC Thr	ACA Thr	AAA Lys	TCA Ser	ATG Met 265	GCT Ala	GCT Ala	CCT Pro	CCA Pro	AGC Ser 270	TGT Cys	814
GGT Gly	CTG Leu	AGC Ser	CCA Pro 275	CTG Leu	CTG Leu	GTC Val	CTG Leu	GTG Val 280	GTA Val	ACC Thr	GCT Ala	CTG Leu	TCC Ser 285	ACC Thr	CTA Leu	862

TTA TCT TTA Leu Ser Leu 290	A ACA GAA AO 1 Thr Glu Th)	CA TCA TAG (nr Ser * 295	CTGCATTAAA A	AAAATACAAT A	ATGGACATGT	916
AAAAAGACAA	AAACCAAGTT	ATCTGTTTCC	TGTTCTCTTG	TATAGCTGAA	ATTCCAGTTT	976
AGGAGCTCAG	TTGAGAAACA	GTTCCATTCA	ACTGGAACAT	$\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}$	CCTTTTAAGA	1036
AAGCTTCTTG	TGATCCTTCG	GGGCTTCTGT	GAAAAACCTG	ATGCAGTGCT	CCATCCAAAC	1096
TCAGAAGGCT	TTGGGATATG	CTGTATTTTA	AAGGGACAGT	TTGTAACTTG	GGCTGTAAAG	1156
CAAACTGGGG	CTGTGTTTTC	GATGATGATG	ATCATCATGA	TCATGATNNN	иииииииии	1216
NNNNNNNNN	NNNNNNNNN	NNNNNGATT	TTAACAGTTT	TACTTCTGGC	CTTTCCTAGC	1276
TAGAGAAGGA	GTTAATATTT	CTAAGGTAAC	TCCCATATCT	CCTTTAATGA	CATTGATTTC	1336
TAATGATATA	AATTTCAGCC	TACATTGATG	CCAAGCTTTT	TTGCCACAAA	GAAGATTCTT	1396
ACCAAGAGTG	GGCTTTGTGG	AAACAGCTGG	TACTGATGTT	CACCTTTATA	TATGTACTAG	1456
CATTTTCCAC	GCTGATGTTT	ATGTACTGTA	AACAGTTCTG	CACTCTTGTA	CAAAAGAAAA	1516
AACACCTGTC	АСАТССАААТ	ATAGTATCTG	TCTTTTCGTC	AAAATAGAGA	GTGGGGAATG	1576
AGTGTGCCGA	TTCAATACCT	CAATCCCTGA	ACGACACTCT	CCTAATCCTA	AGCCTTACCT	1636
GAGTGAGAAG	CCCTTTACCT	AACAAAAGTC	CAATATAGCT	GAAATGTCGC	TCTAATACTC	1696
TTTACACATA	TGAGGTTATA	TGTAGAAAAA	ААТТТТАСТА	CTAAATGATT	TCAACTATTG	1756
GCTTTCTATA	TTTTGAAAGT	AATGATATTG	TCTCATTTTT	TTACTGATGG	TTTAATACAA	1816
AATACACAGA	GCTTGTTTCC	CCTCATAAGT	AGTGTTCGCT	CTGATATGAA	CTTCACAAAT	1876
ACAGCTCATC	AAAAGCAGAC	TCTGAGAAGC	CTCGTGCTGT	AGCAGAAAGT	TCTGCATCAT	1936
GTGACTGTGG	ACAGGCAGGA	GGAAACAGAA	CAGACAAGCA	TTGTCTTTTG	TCATTGCTCG	1996
AAGTGCAAGC	GTGCATACCT	GTGGAGGGAA	CTGGTGGCTG	CTTGTAAATG	TTCTGCAGCA	2056
TCTCTTGACA	CACTTGTCAT	GACACAATCC	AGTACCTTGG	TTTTCAGGTT	ATCTGACAAA	2116
GGCAGCTTTG	ATTGGGACAT	GGAGGCATGG	GCAGGCCGGA	A		2157

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys 1 5 10 15

Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val 20 25 30

Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys 135 Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn 170 Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr 185 Thr Ala Ala Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly 205 Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala 250 Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly 265 Leu Ser Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser 295 290

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 659 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 2..658

- (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..659
 (D) OTHER INFORMATION: /note= "1 to 659 is 1033 to 1691 of Figure 5 Hsgr-21ar"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

G AAT TTG CAG GAC TCC TGC AAG ACG AAT TAC ATC TGC AGA TCT CGC Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg 1 5 10 15								
CTT GCG GAT TTT Leu Ala Asp Phe	TTT ACC AAC T Phe Thr Asn (20	TGC CAG CCA G Cys Gln Pro G 25	AG TCA AGG TCT GTC lu Ser Arg Ser Val 30	AGC 94 Ser				
AGC TGT CTA AAG Ser Cys Leu Lys 35	GAA AAC TAC G Glu Asn Tyr i	GCT GAC TGC C Ala Asp Cys L 40	TC CTC GCC TAC TCG eu Leu Ala Tyr Ser 45	GGG 142 Gly				
CTT ATT GGC ACA Leu Ile Gly Thr 50	GTC ATG ACC (Val Met Thr)	CCC AAC TAC A Pro Asn Tyr I 55	TA GAC TCC AGT AGC le Asp Ser Ser Ser 60	CTC 190 Leu				
AGT GTG GCC CCA Ser Val Ala Pro 65	TGG TGT GAC Trp Cys Asp (TGC AGC AAC A Cys Ser Asn S	GT GGG AAC GAC CTA er Gly Asn Asp Leu 75	GAA 238 Glu				
GAG TGC TTG AAA Glu Cys Leu Lys 80	TTT TTG AAT 1 Phe Leu Asn 1 85	Phe Phe Lys A	AC AAT ACA TGT CTT sp Asn Thr Cys Leu 90	AAA 286 Lys 95				
AAT GCA ATT CAA Asn Ala Ile Gln	GCC TTT GGC A Ala Phe Gly A 100	AAT GGC TCC G Asn Gly Ser A 105	AT GTG ACC GTG TGG sp Val Thr Val Trp 110	CAG 334 Gln				
CCA GCC TTC CCA Pro Ala Phe Pro 115	GTA CAG ACC A	ACC ACT GCC A Thr Thr Ala T 120	CT ACC ACC ACT GCC hr Thr Thr Thr Ala 125	CTC 382 Leu				
CGG GTT AAG AAC Arg Val Lys Asn 130	Lys Pro Leu (GGG CCA GCA G Gly Pro Ala G 135	GG TCT GAG AAT GAA ly Ser Glu Asn Glu 140	ATT 430 lle				
CCC ACT CAT GTT Pro Thr His Val 145	TTG CCA CCG (Leu Pro Pro (150	TGT GCA AAT T Cys Ala Asn L	TA CAG GCA CAG AAG eu Gln Ala Gln Lys 155	CTG 478 Leu				
AAA TCC AAT GTG Lys Ser Asn Val 160	TCG GGC AAT A Ser Gly Asn 7	Thr His Leu C	GT ATT TCC AAT GGT ys Ile Ser Asn Gly 70	AAT 526 Asn 175				
TAT GAA AAA GAA Tyr Glu Lys Glu	GGT CTC GGT (Gly Leu Gly 7 180	GCT TCC AGC C Ala Ser Ser H 185	AC ATA ACC ACA AAA is Ile Thr Thr Lys 190	TCA 574 Ser				
ATG GCT GCT CCT Met Ala Ala Pro 195	CCA AGC TGT (Pro Ser Cys (GGT CTG AGC C Gly Leu Ser P 200	CA CTG CTG GTC CTG ro Leu Leu Val Leu 205	GTG 622 Val				

659

GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA A Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu 210 215

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu
1 10 15

Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser 20 25 30

Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu
35 40

Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser 50 60

Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu 65 70 75 80

Cys Leu Lys Phe Leu Asn Phe Phe Lys Asn Asn Thr Cys Leu Lys Asn 85 90 95

Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro 100 105 110

Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Ala Leu Arg 115 120 125

Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro 130 135 140

Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys 145 150 155

Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr 165 170 175

Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met 180 185 190

Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val 195 200 205

Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu 210 215

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 (B) LOCATION: 3..629
- (ix) FEATURE:
- (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..630
 (D) OTHER INFORMATION: /note= "1 to 630 is 1062 to 1691 of Figure 5 Hsgr-21br"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AC ATC Ile	TGC AG Cys Ar	GA TCT	CGC C Arg L 5	TT GO	CG G la A	AT T	rrr 1 Phe E	TTT A he 1	ACC A	AAC 1 Asn (rgc (Cys (CAG (Gln I	CCA Pro 15	47
GAG TCA Glu Ser	AGG T Arg S	CT GTC Ser Val 20	Ser	AGC 1 Ser (rgt Cys	CTA Leu	AAG Lys 25	GAA Glu	AAC Asn	TAC Tyr	GCT Ala	GAC Asp 30	TGC Cys	95
CTC CTC Leu Leu	GCC T Ala T	TAC TCG Tyr Ser 35	GGG Gly	CTT A	ATT Ile	GGC Gly 40	ACA Thr	GTC Val	ATG Met	ACC Thr	CCC Pro 45	AAC Asn	TAC Tyr	143
ATA GAC	TCC A Ser S 50	AGT AGC Ser Ser	CTC Leu	AGT (Ser V	GTG Val 55	GCC Ala	CCA Pro	TGG Trp	TGT Cys	GAC Asp 60	TGC Cys	AGC Ser	AAC Asn	191
AGT GGG Ser Gly 65	Asn A	GAC CTA Asp Leu	GAA Glu	GAG 1 Glu 0 70	rgc Cys	TTG Leu	AAA Lys	TTT Phe	TTG Leu 75	AAT Asn	TTC Phe	TTC Phe	AAG Lys	239
GAC AAT Asp Asn 80	ACA T	GT CTT Cys Leu	AAA Lys 85	AAT (Asn A	GCA Ala	ATT Ile	CAA Gln	GCC Ala 90	TTT Phe	GGC Gly	AAT Asn	GGC Gly	TCC Ser 95	287
GAT GTG Asp Val	ACC G	TG TGG al Trp 100	CAG Gln	CCA (GCC Ala	TTC Phe	CCA Pro 105	GTA Val	CAG Gln	ACC Thr	ACC Thr	ACT Thr 110	GCC Ala	335
ACT ACC	Thr T	ACT GCC Thr Ala 115	CTC Leu	CGG (Arg \	Val	AAG Lys 120	AAC Asn	AAG Lys	CCC Pro	CTG Leu	GGG Gly 125	CCA Pro	GCA Ala	383
GGG TCT Gly Ser	GAG A Glu A 130	AAT GAA Asn Glu	ATT Ile	Pro 7	ACT Thr 135	CAT His	GTT Val	TTG Leu	CCA Pro	CCG Pro 140	TGT Cys	GCA Ala	AAT Asn	431
TTA CAG Leu Gln 145	Ala G	CAG AAG 31n Lys	Leu	AAA 1 Lys 9 150	TCC Ser	AAT Asn	GTG Val	TCG Ser	GGC Gly 155	AAT Asn	ACA Thr	CAC His	CTC Leu	479
TGT ATT Cys Ile 160	TCC A	AAT GGT Asn Gly	AAT Asn 165	TAT (GAA Glu	AAA Lys	GAA Glu	GGT Gly 170	CTC Leu	GGT Gly	GCT Ala	TCC Ser	AGC Ser 175	527
CAC ATA	ACC A	ACA AAA Thr Lys	TCA Ser	ATG (GCT Ala	GCT Ala	CCT Pro	CCA Pro	AGC Ser	TGT Cys	GGT Gly	CTG Leu	AGC Ser	575

CCA CTG CTG GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu 205

ACA GAA A Thr Glu

- (2) INFORMATION FOR SEQ ID NO:20:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu151015
Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu
20
25
30

Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile 35 40 45

Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser 50 55 60

Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp 65 70 75 80

Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp 85 90 95

Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Ala Thr

Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly 115 120 125

Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu 130 135 140

Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys 145 150 155 160

Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His 165 170 175

Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro 180 185 190

Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr 195 200 205

Glu

(2) INFORMATION FOR SEQ ID NO:21:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1075 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 2445	
<pre>(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 11075 (D) OTHER INFORMATION: /note= "1 to 1075"</pre>	5 is 1255 to 2330
of Figure 5 Hsgr-2"	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
T GGG AAC GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn 1 5	TTC TTC AAG 46 Phe Phe Lys 15
GAC AAT ACA TGT CTT AAA AAT GCA ATT CAA GCC TTT GC Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe G 20 25	GC AAT GGC TCC 94 Ly Asn Gly Ser 30
GAT GTG ACC GTG TGG CAG CCA GCC TTC CCA GTA CAG AC Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Th 35	CC ACC ACT GCC 142 or Thr Thr Ala 45
ACT ACC ACC ACT GCC CTC CGG GTT AAG AAC AAG CCC CTThr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Letter 50	rg ggg cca gca 190 eu gly Pro Ala 50
GGG TCT GAG AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro 65 70 75	CG TGT GCA AAT 238 CO Cys Ala Asn
TTA CAG GCA CAG AAG CTG AAA TCC AAT GTG TCG GGC AA Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Aa 80 85 90	AT ACA CAC CTC 286 on Thr His Leu 95
TGT ATT TCC AAT GGT AAT TAT GAA AAA GAA GGT CTC G	GT GCT TCC AGC 334

CCA CTG CTG GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA
Pro Leu Leu Val Leu Val Thr Ala Leu Ser Thr Leu Leu Ser Leu
130

ACA GAA ACA TCA TAG CTGCATTAAA AAAATACAAT ATGGACATGT AAAAAAGACAA
Thr Glu Thr Ser *

105

382

Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser

CAC ATA ACC ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC

His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser

120

100

115

AAACCAAGTT	ATCTGTTTCC	${\tt TGTTCTCTTG}$	TATAGCTGAA	ATTCCAGTTT	AGGAGCTCAG	545
TTGAGAAACA	GTTCCATTCA	ACTGGAACAT	$\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}$	CCTTTTAAGA	AAGCTTCTTG	605
TGATCCTTCG	GGGCTTCTGT	GAAAAACCTG	ATGCAGTGCT	CCATCCAAAC	TCAGAAGGCT	665
TTGGGATATG	CTGTATTTTA	AAGGGACAGT	TTGTAACTTG	GGCTGTAAAG	CAAACTGGGG	725
CTGTGTTTTC	GATGATGATG	ATCATCATGA	TCATGATNNN	NNNNNNNNN	NNNNNNNNN	785
NNNNNNNNN	NNNNNGATT	TTAACAGTTT	TACTTCTGGC	CTTTCCTAGC	TAGAGAAGGA	845
GTTAATATTT	CTAAGGTAAC	TCCCATATCT	CCTTTAATGA	CATTGATTTC	TAATGATATA	905
AATTTCAGCC	TACATTGATG	CCAAGCTTTT	TTGCCACAAA	GAAGATTCTT	ACCAAGAGTG	965
GGCTTTGTGG	AAACAGCTGG	TACTGATGTT	CACCTTTATA	TATGTACTAG	CATTTTCCAC	1025
GCTGATGTTT	ATGTACTGTA	AACAGTTCTG	CACTCTTGTA	CAAAAGAAAA		1075

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp

Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp

Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr

Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly

Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu

Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys

Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His 105

Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro 115 120 125 115

Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr 140

Glu Thr Ser * 145

(2) INFORMATION FOR SEQ ID NO:23:

	(i)	(<i>I</i> (E	QUENC A) LE 3) TY C) ST O) TO	ENGTH PE: PRANI	H: 10 nucl	059 h leic ESS:	ase ació sino	pai:	cs							
	(ii)	моі	ECUI	LE TY	PE:	cDN2	A									
	(ix)	(2	ATURI A) NA 3) LO	ME/I			128									
oi	(ix) E Fiç	(<i>I</i> (I (I	ATURE A) NA B) LO D) OT	ME/F CATI THER	ON: INFO	11	059			"1 1	co 10)59 i	is 1	272 t	to 233	0
	(xi)	SEÇ	QUENC	CE DI	ESCRI	[PTIC	on: s	SEQ I	ED NO	0:23	:					
AG !	rgc T Cys I 1	rtg A Leu I	AAA T	rrr 7 Phe I	rrg A Leu A 5	AAT T Asn E	TTC T Phe I	TTC A Phe I	AAG (GAC A Asp A	AAT A Asn 1	ACA T	rgt Cys	CTT I	AAA Lys 15	47
AAT Asn	GCA Ala	ATT Ile	CAA Gln	GCC Ala 20	TTT Phe	GGC Gly	AAT Asn	GGC Gly	TCC Ser 25	GAT Asp	GTG Val	ACC Thr	GTG Val	TGG Trp 30	CAG Gln	95
CCA Pro	GCC Ala	TTC Phe	CCA Pro 35	GTA Val	CAG Gln	ACC Thr	ACC Thr	ACT Thr 40	GCC Ala	ACT Thr	ACC Thr	ACC Thr	ACT Thr 45	GCC Ala	CTC Leu	143
CGG Arg	GTT Val	AAG Lys 50	AAC Asn	AAG Lys	CCC Pro	CTG Leu	GGG Gly 55	CCA Pro	GCA Ala	GGG Gly	TCT Ser	GAG Glu 60	AAT Asn	GAA Glu	ATT Ile	191
CCC Pro	ACT Thr 65	CAT His	GTT Val	TTG Leu	CCA Pro	CCG Pro 70	TGT Cys	GCA Ala	AAT Asn	TTA Leu	CAG Gln 75	GCA Ala	CAG Gln	AAG Lys	CTG Leu	239
AAA Lys 80	TCC Ser	AAT Asn	GTG Val	TCG Ser	GGC Gly 85	AAT Asn	ACA Thr	CAC His	CTC Leu	TGT Cys 90	ATT Ile	TCC Ser	AAT Asn	GGT Gly	AAT Asn 95	287
TAT Tyr	GAA Glu	AAA Lys	GAA Glu	GGT Gly 100	CTC Leu	GGT Gly	GCT Ala	TCC Ser	AGC Ser 105	CAC His	ATA Ile	ACC Thr	ACA Thr	AAA Lys 110	TCA Ser	335
ATG Met	GCT Ala	GCT Ala	CCT Pro 115	CCA Pro	AGC Ser	TGT Cys	GGT Gly	CTG Leu 120	AGC Ser	CCA Pro	CTG Leu	CTG Leu	GTC Val 125	CTG Leu	GTG Val	383
GTA Val	ACC Thr	GCT Ala 130	CTG Leu	TCC Ser	ACC Thr	CTA Leu	TTA Leu 135	TCT Ser	TTA Leu	ACA Thr	GAA Glu	ACA Thr 140	TCA Ser	TAG *		428
CTG	CATTA	AAA A	AAAA	raca <i>i</i>	AT AT	rggac	CATG	r aa	AAAG	ACAA	AAA	CAAC	STT	ATCT	GTTTCC	488
TGT	rctci	rTG 1	ratac	GCTG2	AA AT	rtcc <i>i</i>	AGTT	r AGO	GAGC	rcag	TTG	AGAA?	ACA	GTTC	CATTCA	548
ACTO	GGAAC	CAT	rttti	TTTT	т то	сстт)AATI	AAA	AGCT	гстт	GTG	ATCC	ГТТ	GGGG	CTTCTG	608

TGAAAAACCT	GATGCAGTGC	TCCATCCAAA	CTCAGAAGGC	TTTGGGATAT	GCTGTATTTT	668
AAAGGGACAG	TTTGTAACTT	GGGCTGTAAA	GCAAACTGGG	GCTGTGTTTT	CGATGATGAT	728
GATGATCATG	ATGATGATCA	TCATGATCAT	GATGATGATC	ATCATGATCA	TGATGATGAT	788
TTTAACAGTT	TTACTTCTGG	CCTTTCCTAG	CTAGAGAAGG	AGTTAATATT	TCTAAGGTAA	848
CTCCCATATC	TCCTTTAATG	ACATTGATTT	CTAATGATAT	AAATTTCAGC	CTACATTGAT	908
GCCAAGCTTT	TTTGCCACAA	AGAAGATTCT	TACCAAGAGT	GGGCTTTGTG	GAAACAGCTG	968
GTACTGATGT	TCACCTTTAT	ATATGTACTA	GCATTTTCCA	CGCTGATGTT	TATGTACTGT	1028
AAACAGTTCT	GCACTCTTGT	ACAAAAGAAA	A			1059

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
- Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn 1 5 10 15
- Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro
- Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Ala Leu Arg
- Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro 50 60
- Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys
- Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr 85 90 95
- Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met
- Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val 120 115
- Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser 140
- (2) INFORMATION FOR SEQ ID NO:25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids(B) TYPE: amino acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: Gln Ser Cys Ser Thr Lys Tyr Arg Thr Leu
- (2) INFORMATION FOR SEQ ID NO:26:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26: Cys Lys Arg Gly Met Lys Lys Glu Lys Asn
- (2) INFORMATION FOR SEQ ID NO:27:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27: Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val
- (2) INFORMATION FOR SEQ ID NO:28:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids(B) TYPE: amino acid(C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28: Cys Ser Tyr Glu Glu Arg Glu Arg Pro Asn
- (2) INFORMATION FOR SEQ ID NO:29:

	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: peptide	
		SEQUENCE DESCRIPTION: SEQ ID NO:29:	
	Pro 1	Ala Pro Pro Val Gln Thr Thr Thr Ala Thr Thr Thr 5	
(2)	INFO	RMATION FOR SEQ ID NO:30:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:30:	
CTGI		AT TTGCAGGACT C	21
(2)		RMATION FOR SEQ ID NO:31:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:31:	
СТСС	CTCTC'	TA AGCTTCTAAC CACAGCTTGG AGGAGC	36
(2)	INFO	RMATION FOR SEQ ID NO:32:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
CTCCTCTCTA AGCTTCTATG GGCTCAGACC ACAGCTT	37
(2) INFORMATION FOR SEQ ID NO:33:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
CTCCTCTCTA AGCTTCTACT TGTCATCGTC GTCCTTGTAG TCACCACAGC TTGGAGGAGC	60
(2) INFORMATION FOR SEQ ID NO:34:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34: CTCCTCTCTA AGCTTCTACT TGTCATCGTC GTCCTTGTAG TCTGGCTCAG ACCACAGCTT	60
(2) INFORMATION FOR SEQ ID NO:35:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 4232 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 15872978	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	
CATGAAGAAA CCTCAGTAAG TCTCAGACTT GGCCCAAAGG AGCCCAACTA GTTACTCCCT	60
GGTCTGTTAC AGAGGATCTG GCTATTACAC TCAACAGCAA AAATTCAATT CAATCCCGCT	120
AAAGATATAA GAATCACTAG GAAKAATAAG CCAGAACTCA AGACAGAAAT AGCATTAAGT	180

AGTTCCTTCA GTAC	AGTGAG CAGAAGCTGG	CCACTCTACG	ACTCTAWAAG ACTCA	GAAAA 240
GCTTACTAGG GACCY	WCTGGG CATWCCGGTG	TCCTATGTGG	GGATTTCGTA ACGTC	TTTGA 300
GTCAGAAGCT GCCC	TCAAAA TAGTTTCTTC	TCAAAACGGT	TTCAGGCTTT GTTAG	AAAGG 360
GAAGACTTCA CTGC	CACTTT ACCCAGATCA	TCTACCCCAT	CCTTGGAATG AATGG	GGAAG 420
CTTCAGCCAC CCTAG	CCAGGC TCCTAAAATC	ACCAACTTGA	GAGAAAAACT ATAAC	GTTGC 480
TCTACCAGTA CTTC	AGGAGG TTAAAGAAAG	TCACAGAAGA	AAAGAACTCT GGGGA	AAACA 540
GTCAAATTCG GCTA	TTAAGA CATTAGTTAC	AGGCCCCTGT	ACCTCTCCTC TAGAA	ACCCT 600
GGGAGTACAC CCGC	AGAGGA GAGAGAGCCC	AAGCCACCAA	GCAAAGTCAA CCAAT	CTGGC 660
AAAGGGGCGT CCCA	CTGCGG CTTTCAGTCC	AAGAAGTGGA	TCCTGCTGGT TCGCA	GTCTC 720
TCTTCTATCT CCTC	ACTTCC TATTTACCCT	TTGAAGTGGG	TACTGAATAG CCCGT	TCCCA 780
AGCAGAGGCC CTTTC	GTATAC GGGGTGCTAC	AGTCGCCTGG	TGGAAACACC TTGGC	AGAGT 840
TGTTTGGTGC CAGG	ATGGGC CACTGAAGGC	ATCTGCTGTG	GACACACACA CACAC	ACACA 900
CACACACACA CACA	CACACA GAGAGAGGAG	AGAGAAAGAC	ACACGCACGC AGAGA	CACAC 960
GGTCACTGGA ATTC	CATTAG AAAAAAGTGA	GCCGAGCAAG	GGTTAGCGGG AGAAG	ATTTT 1020
TTTGAATCTT GTCT	TCGTCT TGGTGCGAAA	GAAGCGACTC	CAGTCTCTCG TCCTC	GAAGC 1080
TCCGACTGGA TTGT	TCTTGG GCGCTGACAC	CCGTCTGTGG	ATTTCTTTTC TATTT	GCATT 1140
TTATTCCGAC CCCC	TCCCTC GCCGCTTCCT	TCCAGCCCTT	CACTCGCAAA TCGCC	TCTCT 1200
CCCCACCTCC CCAG	GCCCCT CCTGGGAAGC	GCAGGGGAAT	TGGACCCGCG GGGAC	TCACG 1260
CCTTCCCGGA CGAT	TGGAGG GGAGGGCTGA	CCCCAGGACT	GGGCTGTTGG CTTAG	AAAGC 1320
CGATACACAG ATAC	GCGTAT ATTTGATTGT	AGCGGGCAAG	GGGGGCGTCG AGAGG	CAGCA 1380
GCCCATCGCC CGCC	TCTCAC CCCACCCCT	CCAGCCAGAG	GCGAGAATCG CAGGA	CTCGG 1440
GATCTTCATC GGGT	GGACTA GCTGGGATCT	CCGCATTGGA	TTTGGGGCTG ATTAC	CACTG 1500
CTTGGCTATT ATTA	TTGTTG TTGTTACTAC	TATTATTTT	TTTTACCCAA GGGAG	AAAGA 1560
CAAAAAAACG GTGG	GATTTA TTTAAC ATG		A AAC GTC TTC TGC a Asn Val Phe Cys	
	1	Tie Beu Ait	5	204
TTC TTC TTT CTA Phe Phe Phe Leu 10	GAC GAC ACC CTC (Asp Asp Thr Leu 2	CGC TCT TTG Arg Ser Leu 20	GCC AGC CCT TCC Ala Ser Pro Ser	TCC 1661 Ser 25
CTG CAG GGC CCC	GAG CTC CAC GGC Glu Leu His Gly G	TGG CGC CCC Trp Arg Pro 35	CCA GTG GAC TGT Pro Val Asp Cys 40	GTC 1709 Val
CGG GCC AAT GAG Arg Ala Asn Glu 45	CTG TGT GCC GCC (Leu Cys Ala Ala	GAA TCC AAC Glu Ser Asn 50	TGC AGC TCT CGC Cys Ser Ser Arg 55	TAC 1757 Tyr
CGC ACT CTG CGG Arg Thr Leu Arg	CAG TGC CTG GCA (Gln Cys Leu Ala	GGC CGC GAC Gly Arg Asp	CGC AAC ACC ATG Arg Asn Thr Met	CTG 1805 Leu

			60					65					70				
GC A]	CC .	AAC Asn 75	AAG Lys	GAG Glu	TGC Cys	CAG Gln	GCG Ala 80	GCC Ala	TTG Leu	GAG Glu	GTC Val	TTG Leu 85	CAG Gln	GAG Glu	AGC Ser	CCG Pro	1853
L€	rg (eu (TAC Tyr	GAC Asp	TGC Cys	CGC Arg	TGC Cys 95	AAG Lys	CGG Arg	GGC Gly	ATG Met	AAG Lys 100	AAG Lys	GAG Glu	CTG Leu	CAG Gln	TGT Cys 105	1901
CT Le	rg (CAG Gln	ATC Ile	TAC Tyr	TGG Trp 110	AGC Ser	ATC Ile	CAC His	CTG Leu	GGG Gly 115	CTG Leu	ACC Thr	GAG Glu	GGT Gly	GAG Glu 120	GAG Glu	1949
TT Pl	rc ne	TAC Tyr	GAA Glu	GCC Ala 125	TCC Ser	CCC Pro	TAT Tyr	GAG Glu	CCG Pro 130	GTG Val	ACC Thr	TCC Ser	CGC Arg	CTC Leu 135	TCG Ser	GAC Asp	1997
A7 I]	rc i	TTC Phe	AGG Arg 140	CTT Leu	GCT Ala	TCA Ser	ATC Ile	TTC Phe 145	TCA Ser	GGG Gly	ACA Thr	GGG Gly	GCA Ala 150	GAC Asp	CCG Pro	GTG Val	2045
GT Va	al .	AGC Ser 155	GCC Ala	AAG Lys	AGC Ser	AAC Asn	CAT His 160	TGC Cys	CTG Leu	GAT Asp	GCT Ala	GCC Ala 165	AAG Lys	GCC Ala	TGC Cys	AAC Asn	2093
L€	rG eu 70	AAT Asn	GAC Asp	AAC Asn	TGC Cys	AAG Lys 175	AAG Lys	CTG Leu	CGC Arg	TCC Ser	TCC Ser 180	TAC Tyr	ATC Ile	TCC Ser	ATC Ile	TGC Cys 185	2141
A <i>I</i> As	AC sn	CGC Arg	GAG Glu	ATC Ile	TCG Ser 190	CCC Pro	ACC Thr	GAG Glu	CGC Arg	TGC Cys 195	AAC Asn	CGC Arg	CGC Arg	AAG Lys	TGC Cys 200	CAC His	2189
A/ L	AG /s	GCC Ala	CTG Leu	CGC Arg 205	CAG Gln	TTC Phe	TTC Phe	GAC Asp	CGG Arg 210	GTG Val	CCC Pro	AGC Ser	GAG Glu	TAC Tyr 215	ACC Thr	TAC Tyr	2237
CC	GC .	ATG Met	CTC Leu 220	TTC Phe	TGC Cys	TCC Ser	TGC Cys	CAA Gln 225	GAC Asp	CAG Gln	GCG Ala	TGC Cys	GCT Ala 230	GAG Glu	CGC Arg	CGC Arg	2285
CC	g	CAA Gln 235	ACC Thr	ATC Ile	CTG Leu	CCC Pro	AGC Ser 240	TGC Cys	TCC Ser	TAT Tyr	GAG Glu	GAC Asp 245	AAG Lys	GAG Glu	AAG Lys	CCC Pro	2333
As	AC sn 50	TGC Cys	CTG Leu	GAC Asp	CTG Leu	CGT Arg 255	GGC Gly	GTG Val	TGC Cys	CGG Arg	ACT Thr 260	GAC Asp	CAC His	CTG Leu	TGT Cys	CGG Arg 265	2381
T(Se	CC er	CGG Arg	CTG Leu	GCC Ala	GAC Asp 270	TTC Phe	CAT His	GCC Ala	AAT Asn	TGT Cys 275	CGA Arg	GCC Ala	TCC Ser	TAC Tyr	CAG Gln 280	ACG Thr	2429
GT Va	rc al	ACC Thr	AGC Ser	TGC Cys 285	CCT Pro	GCG Ala	GAC Asp	AAT Asn	TAC Tyr 290	CAG Gln	GCG Ala	TGT Cys	CTG Leu	GGC Gly 295	TCT Ser	TAT Tyr	2477
G(A]	CT la	GGC Gly	ATG Met 300	ATT Ile	GGG Gly	TTT Phe	GAC Asp	ATG Met 305	ACA Thr	CCT Pro	AAC Asn	TAT Tyr	GTG Val 310	GAC Asp	TCC Ser	AGC Ser	2525
C(Pi	CC co	ACT Thr	GGC Gly	ATC Ile	GTG Val	GTG Val	TCC Ser	CCC Pro	TGG Trp	TGC Cys	AGC Ser	TGT Cys	CGT Arg	GGC Gly	AGC Ser	GGG Gly	2573

315	320	325	
AAC ATG GAG GAG GAG TGT Asn Met Glu Glu Glu Cys 330 335	GAG AAG TTC CTC AGG Glu Lys Phe Leu Arg 340	GAC TTC ACC GAG AAC Asp Phe Thr Glu Asn 345	2621
CCA TGC CTC CGG AAC GCC Pro Cys Leu Arg Asn Ala 350	ATC CAG GCC TTT GGC Ile Gln Ala Phe Gly 355	AAC GGC ACG AAC GTG Asn Gly Thr Asn Val 360	2669
AAC GTG TCC CCA AAA GGC Asn Val Ser Pro Lys Gly 365	CCC TCG TTC CAG GCC Pro Ser Phe Gln Ala 370	ACC CAG GCC CCT CGG Thr Gln Ala Pro Arg 375	2717
GTG GAG AAG ACG CCT TCT Val Glu Lys Thr Pro Ser 380	TTG CCA GAT GAC CTC Leu Pro Asp Asp Leu 385	AGT GAC AGT ACC AGC Ser Asp Ser Thr Ser 390	2765
TTG GGG ACC AGT GTC ATC Leu Gly Thr Ser Val Ile 395	ACC ACC TGC ACG TCT Thr Thr Cys Thr Ser 400	GTC CAG GAG CAG GGG Val Gln Glu Gln Gly 405	2813
CTG AAG GCC AAC AAC TCC Leu Lys Ala Asn Asn Ser 410 415	AAA GAG TTA AGC ATG Lys Glu Leu Ser Met 420	TGC TTC ACA GAG CTC Cys Phe Thr Glu Leu 425	2861
ACG ACA AAT ATC ATC CCA Thr Thr Asn Ile Ile Pro 430	GGG AGT AAC AAG GTG Gly Ser Asn Lys Val 435	ATC AAA CCT AAC TCA Ile Lys Pro Asn Ser 440	2909
GGC CCC AGC AGA GCC AGA Gly Pro Ser Arg Ala Arg 445	CCG TCG GCT GCC TTG Pro Ser Ala Ala Leu 450	ACC GTG CTG TCT GTC Thr Val Leu Ser Val 455	2957
CTG ATG CTG AAA CTG GCC Leu Met Leu Lys Leu Ala 460		CGAGTC AGAAGATTTT	3008
TGAAAGCTAC GCAGACAAGA AG	CAGCCGCCT GACGAAATGG	AAACACACAC AGACACACAC	3068
ACACCTTGCA AAAAAAAAAT TO	GTTTTTCCC ACCTTGTCGC	TGAACCTGTC TCCTCCCAGG	3128
TTTCTTCTCT GGAGAAGTTT TT	TGTAAACCA AACAGACAAG	CAGGCAGGCA GCCTGAGAGC	3188
TGGCCCAGGG GTCCCCTGGC AC	GGGGAAACT CTGGTGCCGG	GGAGGGCACG AGGCTCTAGA	3248
AATGCCCTTC ACTTTCTCCT GO	GTGTTTTC TCTCTGGACC	CTTCTGAAGC AGAGACCGGA	3308
CAAGAGCCTG CAGCGGAAGG GA	ACTCTGGGC TGTGCCTGAG	GCTGGCTGGG GGCAGGACAA	3368
CACAGCTGCT TCCCCAGGCT G	CCCACTCTG GGGACCCGCT	GGGGGCTGGC AGAGGGCATC	3428
GGTCAGCGGG GCAGCGGGC TO	GGCCATGAG GGTCCACCTT	CAGCCCTTTG GCTTCAAGGA	3488
TGGAGATGGT TTTGCCCTCC C	TCTCTGCCC TCGGGTGGGG	CTGGTGGGTC TGCAGCTGGT	3548
GTGGGAACTT CCCCACGGAT G	GCGGTGGAG GGGGTTCGCA	CCGTGCTGGG CTCCCCCTGA	3608
CTGTAGCACG GAGTGTTGGG G	CTGGGGGCC AGCTCCAGGA	GGGCTTGAGA GCTCAGCCTG	3668
CCTGGGAGAG CCCTTGTGGC GA	AGGCATTAA AACTTGGGCA	CCAGCTTCTT TCTCGGTGGC	3728
AGAAATTTTG AAGTCAGAGA G	AAACGGTCC TTTGTTGGCT	TCTTTGCTTT CTCGTGGGTC	3788

CTTTGGCAGG	CCTCCCTTTG	GGGAGAGGGA	GGGGAGAGAC	CACAGCCGGG	TGTGTGTCTG	3848
CAGCACCGTG	GGCCCTCAAG	CTTTCCTGCT	GTCTTCTCCC	TCCTCCTCCT	TTCCCCTTTC	3908
тстттсстса	TTTCCTAGAC	GTACGTCAAC	TGTATGTACA	TACCGGGGCT	CCTCTCCTAA	3968
CATATATGTA	TATACACATC	CATATACATA	TATTGTGTGG	TTTCCCCTTT	CTTTCCTTTT	4028
TTTAAGCAAC	AAAACTATGG	AAATAATACC	CCAACAGATG	AGCGAAAATG	TATTATTGTA	4088
AAGTTTATTT	TTTTTAATAC	TGTTGTCTAT	AATGGGGAAA	AAGGACATTG	GCCCGCAGT	4148
GCCCTGCCCC	AGTCAGCCTG	GCTGGGCTCT	GGTGGGGGCT	CCTGATCCGC	ATCCAAGCTT	4208
AACCAAGGCT	CCAATAAACG	TGCG				4232

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 464 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser Cys Gln Asp Gln Ala Cys Ala Glu Arg Arg Gln Thr Ile Leu Pro Ser 235 Cys Ser Tyr Glu Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg Gly Val Cys Arg Thr Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe His Ala Asn Cys Arg Ala Ser Tyr Gln Thr Val Thr Ser Cys Pro Ala Asp 285 280 Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp 295 Met Thr Pro Asn Tyr Val Asp Ser Ser Pro Thr Gly Ile Val Val Ser Pro Trp Cys Ser Cys Arg Gly Ser Gly Asn Met Glu Glu Cys Glu 330 325 Lys Phe Leu Arg Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile Gln Ala Phe Gly Asn Gly Thr Asn Val Asn Val Ser Pro Lys Gly Pro Ser Phe Gln Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu 375 Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr Thr Cys Thr Ser Val Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ile Pro Gly Ser Asn Lys Val Ile Lys Pro Asn Ser Gly Pro Ser Arg Ala Arg Pro 440 Ser Ala Ala Leu Thr Val Leu Ser Val Leu Met Leu Lys Leu Ala Leu

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1991 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 203..1402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3/:												
CAAGTCAAAG GTTTAATCAT GATCCAAGAG CCCAGAGAGA CTTTAGGACA ATAATAGGAA												
TAAAGCAAGG (CCACAGGCT C	CAGCTCCTG AT	GCCCAGAT GT	TCGGCAGG ATCC	GGGGAC 120							
AGGGCAGTGC A	AGGCAGTAGT T	TTCCATCCT CC	ATCCAGGG GA	GGAGCGAG GGGAG	CGCGG 180							
AGCCCGGCGC C	CTACAGCTCG CO	C ATG GTG CG Met Val Ar 1	C CCC CTG A g Pro Leu A 5	AC CCG CGA CCG Asn Pro Arg Pro	CTG 232 Leu 10							
CCG CCC GTA Pro Pro Val	GTC CTG ATG Val Leu Met 15	TTG CTG CTG Leu Leu Leu	CTG CTG CC Leu Leu Pr 20	eG CCG TCG CCG to Pro Ser Pro 25	CTG 280 Leu							
CCT CTC GCA Pro Leu Ala	GCC GGA GAC Ala Gly Asp 30	CCC CTT CCC Pro Leu Pro 35	Thr Glu Se	GC CGA CTC ATG er Arg Leu Met 40	AAC 328 Asn							
AGC TGT CTC Ser Cys Leu 45	CAG GCC AGG Gln Ala Arg	AGG AAG TGC Arg Lys Cys 50	CAG GCT GA Gln Ala As	AT CCC ACC TGC sp Pro Thr Cys 55	AGT 376 Ser							
GCT GCC TAC Ala Ala Tyr 60	CAC CAC CTG His His Leu	GAT TCC TGC Asp Ser Cys 65	Thr Ser Se	GC ATA AGC ACC er Ile Ser Thr 0	CCA 424 Pro							
CTG CCC TCA Leu Pro Ser 75	GAG GAG CCT Glu Glu Pro 80	TCG GTC CCT Ser Val Pro	GCT GAC TG Ala Asp Cy 85	GC CTG GAG GCA vs Leu Glu Ala	GCA 472 Ala 90							
CAG CAA CTC Gln Gln Leu	AGG AAC AGC Arg Asn Ser 95	TCT CTG ATA Ser Leu Ile	GGC TGC AT Gly Cys Me 100	TG TGC CAC CGG et Cys His Arg 105	CGC 520 Arg							
ATG AAG AAC Met Lys Asn	CAG GTT GCC Gln Val Ala 110	TGC TTG GAC Cys Leu Asp 115	lle Tyr Tr	GG ACC GTT CAC TP Thr Val His 120	CGT 568 Arg							
GCC CGC AGC Ala Arg Ser 125	CTT GGT AAC Leu Gly Asn	TAT GAG CTG Tyr Glu Leu 130	GAT GTC TC Asp Val Se	CC CCC TAT GAA er Pro Tyr Glu 135	GAC 616 Asp							
ACA GTG ACC Thr Val Thr 140	AGC AAA CCC Ser Lys Pro	TGG AAA ATG Trp Lys Met 145	AAT CTC AG Asn Leu Se 15	GC AAA CTG AAC er Lys Leu Asn 00	ATG 664 Met							
CTC AAA CCA Leu Lys Pro 155	GAC TCA GAC Asp Ser Asp 160	CTC TGC CTC Leu Cys Leu	AAG TTT GC Lys Phe Al 165	CC ATG CTG TGT a Met Leu Cys	ACT 712 Thr 170							
CTC AAT GAC Leu Asn Asp	AAG TGT GAC Lys Cys Asp 175	CGG CTG CGC Arg Leu Arg	AAG GCC TA Lys Ala Ty 180	AC GGG GAG GCG or Gly Glu Ala 185	TGC 760 Cys							
TCC GGG CCC Ser Gly Pro	CAC TGC CAG His Cys Gln 190	CGC CAC GTC Arg His Val 195	. Cys Leu Ar	GG CAG CTG CTC cg Gln Leu Leu 200	ACT 808 Thr							

TTC TTC GAG AAG Phe Phe Glu Lys 205	GCC GCC GAG Ala Ala Glu	CCC CAC GCG Pro His Ala 210	CAG GGC CTG C Gln Gly Leu I 215	CTA CTG TGC Leu Leu Cys	856
CCA TGT GCC CCC Pro Cys Ala Pro 220	AAC GAC CGG Asn Asp Arg 225	GGC TGC GGG Gly Cys Gly	GAG CGC CGG C Glu Arg Arg A 230	CGC AAC ACC Arg Asn Thr	904
ATC GCC CCC AAC Ile Ala Pro Asn 235	TGC GCG CTG Cys Ala Leu 240	CCG CCT GTG Pro Pro Val	GCC CCC AAC 1 Ala Pro Asn 0 245	rGC CTG GAG Cys Leu Glu 250	952
CTG CGG CGC CTC Leu Arg Arg Leu	TGC TTC TCC Cys Phe Ser 255	GAC CCG CTT Asp Pro Leu 260	TGC AGA TCA C Cys Arg Ser A	CGC CTG GTG Arg Leu Val 265	1000
GAT TTC CAG ACC Asp Phe Gln Thr 270	His Cys His	CCC ATG GAC Pro Met Asp 275	Ile Leu Gly 7	ACT TGT GCA Thr Cys Ala 280	1048
ACA GAG CAG TCC Thr Glu Gln Ser 285	AGA TGT CTA Arg Cys Leu	CGA GCA TAC Arg Ala Tyr 290	CTG GGG CTG A Leu Gly Leu 1 295	ATT GGG ACT lle Gly Thr	1096
GCC ATG ACC CCC Ala Met Thr Pro 300	AAC TTT GCC Asn Phe Ala 305	AGC AAT GTC Ser Asn Val	AAC ACC AGT C Asn Thr Ser V 310	GTT GCC TTA /al Ala Leu	1144
AGC TGC ACC TGC Ser Cys Thr Cys 315	CGA GGC AGT Arg Gly Ser 320	GGC AAC CTG Gly Asn Leu	CAG GAG GAG T Gln Glu Glu G 325	TGT GAA ATG Cys Glu Met 330	1192
CTG GAA GGG TTC Leu Glu Gly Phe	TTC TCC CAC Phe Ser His 335	AAC CCC TGC Asn Pro Cys 340	CTC ACG GAG C Leu Thr Glu A	GCC ATT GCA Ala Ile Ala 345	1240
GCT AAG ATG CGT Ala Lys Met Arg 350	Phe His Ser	CAA CTC TTC Gln Leu Phe 355	Ser Gln Asp 7	rGG CCA CAC Trp Pro His 360	1288
CCT ACC TTT GCT Pro Thr Phe Ala 365	GTG ATG GCA Val Met Ala	CAC CAG AAT His Gln Asn 370	GAA AAC CCT C Glu Asn Pro A 375	GCT GTG AGG Ala Val Arg	1336
CCA CAG CCC TGG Pro Gln Pro Trp 380	GTG CCC TCT Val Pro Ser 385	Leu Phe Ser	TGC ACG CTT C Cys Thr Leu I 390	CCC TTG ATT Pro Leu Ile	1384
CTG CTC CTG AGC Leu Leu Leu Ser 395		CTGGACT TCCCC	CAGGGC CCTCTTC	eccc	1432
TCCACCACAC CCAG	GTGGAC TTGCA	GCCCA CAAGGG	TGA GGAAAGGA	CA GCAGCAGGAA	1492
GGAGGTGCAG TGCG	CAGATG AGGGC	ACAGG AGAAGCT	TAAG GGTTATGAG	CC TCCAGATCCT	1552
TACTGGTCCA GTCC	TCATTC CCTCC	ACCCC ATCTCC	ACTT CTGATTCAT	rg ctgcccctcc	1612
TTGGTGGCCA CAAT	TTAGCC ATGTC	ATCTG GTGGTG	ACCA GCTCCACCA	AA GCCCCTTTGT	1672
GAGCCCTTCC TCTT	GACTAC CAGGA	TCACC AGAATC	TAAT AAGTTAGCO	TTCTCTATTG	1732
CATTCCAGAT TAGG	GTTAGG GTAGG	GAGGA CTGGGT	GTTC TGAGGCAG	CC TAGAAAGTCA	1792

TTCTCCTTTG	TGAAGAAGGC	TCCTGCCCCC	TCGTCTCCTC	CTCTGAGTGG	AGGATGGAAA	1852
ACTACTGCCT	GCACTGCCCT	GTCCCCGGAT	CCTGCCGAAC	ATCTGGGCAT	CAGGAGCTGG	1912
AGCCTGTGGG	CCTTGCTTTA	TTCCTATTAT	TGTCCTAAAG	TCTCTCTGGG	CTCTTGGATC	1972
ATGATTAAAC	CTTTGACTG					1991

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 400 amino acids

 (B) TYPE: amino acid

 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vi) SECTIFNOR DESCRIPTION: SEC ID NO.38:

	()	(i) (SEQUE	ENCE	DESC	RIPT	: NOI	SEÇ) ID	NO:3	88:				
Met 1	Val	Arg	Pro	Leu 5	Asn	Pro	Arg	Pro	Leu 10	Pro	Pro	Val	Val	Leu 15	Met
Leu	Leu	Leu	Leu 20	Leu	Pro	Pro	Ser	Pro 25	Leu	Pro	Leu	Ala	Ala 30	Gly	Asp
Pro	Leu	Pro 35	Thr	Glu	Ser	Arg	Leu 40	Met	Asn	Ser	Cys	Leu 45	Gln	Ala	Arg
Arģ	Lys 50	Cys	Gln	Ala	Asp	Pro 55	Thr	Cys	Ser	Ala	Ala 60	Tyr	His	His	Leu
Asp 65	Ser	Cys	Thr	Ser	Ser 70	Ile	Ser	Thr	Pro	Leu 75	Pro	Ser	Glu	Glu	Pro 80
Ser	Val	Pro	Ala	Asp 85	Cys	Leu	Glu	Ala	Ala 90	Gln	Gln	Leu	Arg	Asn 95	Ser
Ser	Leu	Ile	Gly 100	Cys	Met	Cys	His	Arg 105	Arg	Met	Lys	Asn	Gln 110	Val	Ala
Cys	Leu	Asp 115	Ile	Tyr	Trp	Thr	Val 120	His	Arg	Ala	Arg	Ser 125	Leu	Gly	Asn
Tyr	Glu 130	Leu	Asp	Val	Ser	Pro 135	Tyr	Glu	Asp	Thr	Val 140	Thr	Ser	Lys	Pro
Trp 145	Lys	Met	Asn	Leu	Ser 150	Lys	Leu	Asn	Met	Leu 155	Lys	Pro	Asp	Ser	Asp 160
Leu	Cys	Leu	Lys	Phe 165	Ala	Met	Leu	Cys	Thr 170	Leu	Asn	Asp	Lys	Cys 175	Asp
Arg	Leu	Arg	Lys 180	Ala	Tyr	Gly	Glu	Ala 185	Cys	Ser	Gly	Pro	His 190	Cys	Gln
Arg	His	Val 195	Cys	Leu	Arg	Gln	Leu 200	Leu	Thr	Phe	Phe	Glu 205	Lys	Ala	Ala
Glu	Pro 210	His	Ala	Gln	Gly	Leu 215	Leu	Leu	Cys	Pro	Cys 220	Ala	Pro	Asn	Asp
Arg	Gly	Cys	Gly	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala

225					230					235					240
Leu	Pro	Pro	Val	Ala 245	Pro	Asn	Cys	Leu	Glu 250	Leu	Arg	Arg	Leu	Cys 255	Phe
Ser	Asp	Pro	Leu 260	Cys	Arg	Ser	Arg	Leu 265	Val	Asp	Phe	Gln	Thr 270	His	Cys
His	Pro	Met 275	Asp	Ile	Leu	Gly	Thr 280	Cys	Ala	Thr	Glu	Gln 285	Ser	Arg	Cys
Leu	Arg 290	Ala	Tyr	Leu	Gly	Leu 295	Ile	Gly	Thr	Ala	Met 300	Thr	Pro	Asn	Phe
Ala 305	Ser	Asn	Val	Asn	Thr 310	Ser	Val	Ala	Leu	Ser 315	Cys	Thr	Cys	Arg	Gly 320
Ser	Gly	Asn	Leu	Gln 325	Glu	Glu	Cys	Glu	Met 330	Leu	Glu	Gly	Phe	Phe 335	Ser
His	Asn	Pro	Cys 340	Leu	Thr	Glu	Ala	Ile 345	Ala	Ala	Lys	Met	Arg 350	Phe	His
Ser	Gln	Leu 355	Phe	Ser	Gln	Asp	Trp 360	Pro	His	Pro	Thr	Phe 365	Ala	Val	Met
Ala	His 370	Gln	Asn	Glu	Asn	Pro 375	Ala	Val	Arg	Pro	Gln 380	Pro	Trp	Val	Pro
Ser 385	Leu	Phe	Ser	Cys	Thr 390	Leu	Pro	Leu	Ile	Leu 395	Leu	Leu	Ser	Leu	Trp 400
(2)	INFO	ORMAT	rion	FOR	SEQ	ID 1	10:39) :							
	(i)	SEC	HENC	E CE	IARAC	TER	STIC	cs:							

- - EQUENCE CHARACTERISTICS:

 (A) LENGTH: 2215 base pairs

 (B) TYPE: nucleic acid

 (C) STRANDEDNESS: single

 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 684..2063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCGGCCGCGT	CGACCTTGAC	CATGCAGACA	CTTTTTCAGG	CCTCTGTCTG	GTGTGAAGTT	60
GGCAGATACA	AGCAAGGCCC	GAAAGGGGTC	TCAGCTTCTC	TCTCCTGGGC	CTCCTGGACT	120
GAGTTAGGCT	TGCTTCTGGT	TGTCTTCTAA	AGGCACGGTG	ATACAGAATG	ATGAGACTAG	180
GCTGGAGGGG	GCTTTCTGCT	TCTCTGTGTG	TGACCTTGAG	TTATCTCCCT	TCGTTGGATC	240
CGAGCTTTCC	TGGAATATGA	TGTTGAATAT	GAATATGAGT	TCTGCCTAAG	GTCCAGACAG	300
GCTCTGAGGG	TTAACTGACT	TTTGGAGCCT	тсааатсаат	ACCTTGGATG	GAGTGGGGGT	360
TTGTCCAATG	GGAGTTGAGG	CAAGATCCCT	TTGCATAAGC	CTTGCCACAT	CATGTTGAAG	420

CCATGCCATT CTGTC	CTGGAC TATTGGCAT	C TTACCTTTCC	AGCAGTTTCA GTGAAGGCC	CT 480
TCCTGGATTT ATCAT	TTCTGT GTTCCACTG	C CTAGGATTGT	GCTCAAGAGG AAATGAATG	ST 540
GAACCATGGT TGTAC	GGGAG TATGGCCAA	C CAGGTTGGGT	CTGTGTTGAC CTTGGTCTT	rg 600
GTGTTCTTTT GTGT	AAAGTG GGTGAGAAG	T TCCTTCAAAC	CTTAGGCCTA CATTGGGGT	rc 660
AGAGACTGTG GTGGC	CCCTCA TTC ATG C Met L 1	TT GTC TTC CO eu Val Phe Pi	CT TCC CAC TAC CCA ro Ser His Tyr Pro 5	710
GAC GAA ACC CTC Asp Glu Thr Leu 10	CGC TCT TTG GCC Arg Ser Leu Ala 15	AGC CCT TCC Ser Pro Ser 20	TCC CTG CAG GGC TCT Ser Leu Gln Gly Ser 25	758
GAG CTC CAC GGC Glu Leu His Gly	TGG CGC CCC CAA Trp Arg Pro Gln 30	GTG GAC TGT Val Asp Cys 35	GTC CGG GCC AAT GAG Val Arg Ala Asn Glu 40	806
CTG TGT GCG GCT Leu Cys Ala Ala 45	GAA TCC AAC TGC Glu Ser Asn Cys	AGC TCC AGG Ser Ser Arg 50	TAC CGC ACC CTT CGG Tyr Arg Thr Leu Arg 55	854
CAG TGC CTG GCA Gln Cys Leu Ala 60	GGC CGG GAT CGC Gly Arg Asp Arg 65	Asn Thr Met	CTG GCC AAT AAG GAG Leu Ala Asn Lys Glu 70	902
TGC CAG GCA GCC Cys Gln Ala Ala 75	CTG GAG GTC TTG Leu Glu Val Leu 80	CAG GAA AGC Gln Glu Ser	CCA CTG TAT GAC TGC Pro Leu Tyr Asp Cys 85	950
CGC TGC AAG CGG Arg Cys Lys Arg 90	GGC ATG AAG AAG Gly Met Lys Lys 95	GAG CTG CAG Glu Leu Gln 100	TGT CTG CAG ATC TAC Cys Leu Gln Ile Tyr 105	998
TGG AGC ATC CAT Trp Ser Ile His	CTG GGG CTG ACA Leu Gly Leu Thr 110	GAG GGT GAG Glu Gly Glu 115	GAG TTC TAT GAA GCT Glu Phe Tyr Glu Ala 120	1046
TCC CCC TAT GAG Ser Pro Tyr Glu 125	CCT GTG ACC TCG Pro Val Thr Ser	CGC CTC TCG Arg Leu Ser 130	GAC ATC TTC AGG CTC Asp Ile Phe Arg Leu 135	1094
GCT TCA ATC TTC Ala Ser Ile Phe 140	TCA GGG ACA GGG Ser Gly Thr Gly 145	Thr Asp Pro	GCG GTC AGT ACC AAA Ala Val Ser Thr Lys 150	1142
AGC AAC CAC TGC Ser Asn His Cys 155	CTG GAT GCC GCC Leu Asp Ala Ala 160	AAG GCC TGC Lys Ala Cys	AAC CTG AAT GAC AAC Asn Leu Asn Asp Asn 165	1190
TGC AAG AAG CTT Cys Lys Lys Leu 170	CGC TCC TCT TAT Arg Ser Ser Tyr 175	ATC TCC ATC Ile Ser Ile 180	TGC AAC CGT GAG ATC Cys Asn Arg Glu Ile 185	1238
TCT CCC ACC GAA Ser Pro Thr Glu	CGC TGC AAC CGC Arg Cys Asn Arg 190	CGC AAG TGC Arg Lys Cys 195	CAC AAG GCT CTG CGC His Lys Ala Leu Arg 200	1286
CAG TTC TTT GAC Gln Phe Phe Asp 205	CGT GTG CCC AGC Arg Val Pro Ser	GAG TAT ACC Glu Tyr Thr 210	TAC CGC ATG CTC TTC Tyr Arg Met Leu Phe 215	1334

TGC Cys	TCC Ser	TGT Cys 220	CAG Gln	GAC Asp	CAG Gln	GCA Ala	TGT Cys 225	GCT Ala	GAG Glu	CGT Arg	CGC Arg	CGG Arg 230	CAA Gln	ACC Thr	ATC Ile	:	1382
CTG Leu	CCC Pro 235	AGT Ser	TGC Cys	TCC Ser	TAT Tyr	GAG Glu 240	GAC Asp	AAG Lys	GAG Glu	AAG Lys	CCC Pro 245	AAC Asn	TGC Cys	CTG Leu	GAC Asp	:	1430
CTG Leu 250	CGC Arg	AGC Ser	CTG Leu	TGT Cys	CGT Arg 255	ACA Thr	GAC Asp	CAC His	CTG Leu	TGC Cys 260	CGG Arg	TCC Ser	CGA Arg	CTG Leu	GCA Ala 265	į	1478
GAT Asp	TTC Phe	CAC His	GCC Ala	AAC Asn 270	TGT Cys	CGA Arg	GCC Ala	TCC Ser	TAC Tyr 275	CGG Arg	ACA Thr	ATC Ile	ACC Thr	AGC Ser 280	TGT Cys	:	1526
CCT Pro	GCG Ala	GAC Asp	AAC Asn 285	TAC Tyr	CAG Gln	GCA Ala	TGT Cys	CTG Leu 290	GGC Gly	TCC Ser	TAT Tyr	GCT Ala	GGC Gly 295	ATG Met	ATT Ile	-	1574
GGG Gly	TTT Phe	GAT Asp 300	ATG Met	ACA Thr	CCC Pro	AAC Asn	TAT Tyr 305	GTG Val	GAC Asp	TCC Ser	AAC Asn	CCC Pro 310	ACG Thr	GGC Gly	ATC Ile	:	1622
GTG Val	GTG Val 315	TCT Ser	CCC Pro	TGG Trp	TGC Cys	AAT Asn 320	TGT Cys	CGT Arg	GGC Gly	AGT Ser	GGG Gly 325	AAC Asn	ATG Met	GAA Glu	GAA Glu	-	1670
GAG Glu 330	TGT Cys	GAG Glu	AAG Lys	TTC Phe	CTC Leu 335	AGG Arg	GAC Asp	TTC Phe	ACG Thr	GAA Glu 340	AAC Asn	CCA Pro	TGC Cys	CTC Leu	CGG Arg 345	:	1718
AAT Asn	GCC Ala	ATT Ile	CAG Gln	GCC Ala 350	TTT Phe	GGT Gly	AAT Asn	GGC Gly	ACA Thr 355	GAT Asp	GTG Val	AAC Asn	ATG Met	TCT Ser 360	CCC Pro	:	1766
AAA Lys	GGC Gly	CCC Pro	TCA Ser 365	CTC Leu	CCA Pro	GCT Ala	ACC Thr	CAG Gln 370	GCC Ala	CCT Pro	CGG Arg	GTG Val	GAG Glu 375	AAG Lys	ACT Thr	:	1814
CCT Pro	TCA Ser	CTG Leu 380	CCA Pro	GAT Asp	GAC Asp	CTC Leu	AGT Ser 385	GAC Asp	AGC Ser	ACC Thr	AGC Ser	CTG Leu 390	GGG Gly	ACC Thr	AGT Ser	:	1862
GTC Val	ATC Ile 395	ACC Thr	ACC Thr	TGC Cys	ACA Thr	TCT Ser 400	ATC Ile	CAG Gln	GAG Glu	CAA Gln	GGG Gly 405	CTG Leu	AAG Lys	GCC Ala	AAC Asn	:	1910
AAC Asn 410	TCC Ser	AAA Lys	GAG Glu	TTA Leu	AGC Ser 415	ATG Met	TGC Cys	TTC Phe	ACA Thr	GAG Glu 420	CTC Leu	ACG Thr	ACA Thr	AAC Asn	ATC Ile 425	:	1958
AGT Ser	CCA Pro	GGG Gly	AGT Ser	AAA Lys 430	AAG Lys	GTG Val	ATC Ile	AAA Lys	CTT Leu 435	AAC Asn	TCA Ser	GGC Gly	TCC Ser	AGC Ser 440	AGA Arg	:	2006
GCC Ala	AGA Arg	CTG Leu	TCG Ser 445	GCT Ala	GCC Ala	TTG Leu	ACT Thr	GCC Ala 450	CTC Leu	CCA Pro	CTC Leu	CTG Leu	ATG Met 455	CTG Leu	ACC Thr	:	2054
		TTG Leu 460	TAG	GCCT'	rtg (GAACO	CCAG	CA C	AAAA(TTC:	r TC	AAGC	AACC			:	2103

2163

2215

CAGATATGAA CTCCCGCCTG ACAAAATGGA AACACACGCA TACACACATG CCACACACAG ACACACACA AGACACACA ACACACACA ATACAGACGT CGACGCGGCC GC (2) INFORMATION FOR SEQ ID NO:40: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 460 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40: Met Leu Val Phe Pro Ser His Tyr Pro Asp Glu Thr Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Ser Glu Leu His Gly Trp Arg Pro Gln Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile Phe Ser Gly Thr Gly Thr Asp Pro Ala Val Ser Thr Lys Ser Asn His Cys Leu Asp Ala 150 Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Arg Val Pro 200 Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser Cys Gln Asp Gln Ala 215 Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro Ser Cys Ser Tyr Glu

Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg Ser Leu Cys Arg Thr

250

Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe His Ala Asn Cys Arg 265 Ala Ser Tyr Arg Thr Ile Thr Ser Cys Pro Ala Asp Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp Met Thr Pro Asn Tyr Val Asp Ser Asn Pro Thr Gly Ile Val Val Ser Pro Trp Cys Asn 315 Cys Arg Gly Ser Gly Asn Met Glu Glu Glu Cys Glu Lys Phe Leu Arg 330 Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile Gln Ala Phe Gly Asn Gly Thr Asp Val Asn Met Ser Pro Lys Gly Pro Ser Leu Pro Ala 360 Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr Thr Cys Thr Ser Ile Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys Glu Leu Ser Met 405 410 Cys Phe Thr Glu Leu Thr Thr Asn Ile Ser Pro Gly Ser Lys Lys Val Ile Lys Leu Asn Ser Gly Ser Ser Arg Ala Arg Leu Ser Ala Ala Leu 440 Thr Ala Leu Pro Leu Leu Met Leu Thr Leu Ala Leu 455

- (2) INFORMATION FOR SEQ ID NO:41:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1699 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 67..1257
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCGGCCGCGT CGACCGACGC CCAGCACAGG CAGAGCGCTG CCGGGTCCGC GGCGTCCAGA 60

CCCGCC ATG GGG CTC TCC CGG AGC CCG CGA CCG CCG CCG CTA GTG ATC

Met Gly Leu Ser Arg Ser Pro Arg Pro Pro Pro Leu Val Ile

1 5 10

CTG Leu 15	CTA Leu	CTG Leu	GTG Val	CTG Leu	TCG Ser 20	CTG Leu	TGG Trp	CTA Leu	CCC Pro	CTT Leu 25	GGA Gly	ACA Thr	GGA Gly	AAC Asn	TCC Ser 30	156
CTT Leu	CCC Pro	ACA Thr	GAG Glu	AAC Asn 35	AGG Arg	CTT Leu	GTG Val	AAC Asn	AGC Ser 40	TGT Cys	ACC Thr	CAG Gln	GCC Ala	AGA Arg 45	AAA Lys	204
AAA Lys	TGC Cys	GAG Glu	GCT Ala 50	AAT Asn	CCC Pro	GCT Ala	TGC Cys	AAG Lys 55	GCT Ala	GCC Ala	TAC Tyr	CAG Gln	CAC His 60	CTG Leu	GAC Asp	252
TCC Ser	TGC Cys	ACC Thr 65	CCC Pro	AGT Ser	CTC Leu	AGC Ser	AGT Ser 70	CCA Pro	CTG Leu	CCC Pro	TCA Ser	GGG Gly 75	GAG Glu	TCT Ser	GCC Ala	300
ACA Thr	TCT Ser 80	GCA Ala	GCG Ala	TGC Cys	CTT Leu	GAA Glu 85	GCA Ala	GCA Ala	CAG Gln	CAA Gln	CTC Leu 90	AGG Arg	AAC Asn	AGC Ser	TCT Ser	348
CTC Leu 95	ATA Ile	GAC Asp	TGC Cys	AGG Arg	TGC Cys 100	CAC His	CGG Arg	CGC Arg	ATG Met	AAG Lys 105	CAC His	CAA Gln	GCT Ala	ACC Thr	TGT Cys 110	396
CTG Leu	GAC Asp	ATT Ile	TAT Tyr	TGG Trp 115	ACC Thr	GTT Val	CAC His	CCT Pro	GTC Val 120	CGA Arg	AGC Ser	CTT Leu	GGT Gly	GAC Asp 125	TAC Tyr	444
GAG Glu	TTG Leu	GAC Asp	GTC Val 130	TCA Ser	CCC Pro	TAT Tyr	GAA Glu	GAC Asp 135	ACA Thr	GTG Val	ACC Thr	AGC Ser	AAA Lys 140	CCC Pro	TGG Trp	492
AAA Lys	ATG Met	AAT Asn 145	CTC Leu	AGC Ser	AAG Lys	CTG Leu	AGC Ser 150	ATG Met	CTC Leu	AAA Lys	CCA Pro	GAC Asp 155	TCC Ser	GAC Asp	CTC Leu	540
TGC Cys	CTC Leu 160	AAA Lys	TTT Phe	GCT Ala	ATG Met	CTG Leu 165	TGT Cys	ACT Thr	CTT Leu	AAC Asn	GAC Asp 170	AAG Lys	TGC Cys	GAC Asp	CGC Arg	588
CTC Leu 175	CGA Arg	AAG Lys	GCC Ala	TAC Tyr	GGG Gly 180	GAG Glu	GCG Ala	TGC Cys	TCA Ser	GGG Gly 185	ATC Ile	CGC Arg	TGC Cys	CAG Gln	CGC Arg 190	636
CAC His	CTC Leu	TGC Cys	CTA Leu	GCT Ala 195	CAG Gln	CTG Leu	CGC Arg	TCC Ser	TTC Phe 200	TTC Phe	GAG Glu	AAG Lys	GCG Ala	GCA Ala 205	GAG Glu	684
TCC Ser	CAC His	GCT Ala	CAG Gln 210	GGC Gly	CTG Leu	CTG Leu	CTG Leu	TGT Cys 215	CCC Pro	TGT Cys	GCA Ala	CCC Pro	GAA Glu 220	GAT Asp	GCG Ala	732
GGC Gly	TGT Cys	GGG Gly 225	GAG Glu	CGC Arg	CGG Arg	CGC Arg	AAC Asn 230	ACC Thr	ATC Ile	GCC Ala	CCC Pro	AGT Ser 235	TGC Cys	GCC Ala	CTC Leu	780
CCG Pro	TCT Ser 240	GTG Val	GCC Ala	CCC Pro	AAC Asn	TGC Cys 245	CTA Leu	GAT Asp	CTT Leu	CGG Arg	AGC Ser 250	TTC Phe	TGC Cys	CGT Arg	GCG Ala	828
GAC Asp 255	CCT Pro	CTG Leu	TGC Cys	AGA Arg	TCA Ser 260	CGC Arg	CTG Leu	ATG Met	GAC Asp	TTC Phe 265	CAG Gln	ACC Thr	CAC His	TGC Cys	CAC His 270	876

CCT Pro	ATG Met	GAC Asp	ATC Ile	CTC Leu 275	GGG Gly	ACT Thr	TGT Cys	GCA Ala	ACT Thr 280	GAG Glu	CAG Gln	TCC Ser	AGA Arg	TGT Cys 285	CTG Leu	924
CGG Arg	GCA Ala	TAC Tyr	CTG Leu 290	GGG Gly	CTA Leu	ATT Ile	GGG Gly	ACT Thr 295	GCC Ala	ATG Met	ACC Thr	CCA Pro	AAC Asn 300	TTC Phe	ATC Ile	972
AGC Ser	AAG Lys	GTC Val 305	AAC Asn	ACT Thr	ACT Thr	GTT Val	GCC Ala 310	TTA Leu	GGC Gly	TGT Cys	ACC Thr	TGC Cys 315	CGA Arg	GGC Gly	AGT Ser	1020
GGC Gly	AAC Asn 320	CTG Leu	CAG Gln	GAC Asp	GAG Glu	TGT Cys 325	GAA Glu	CAG Gln	CTG Leu	GAA Glu	AAG Lys 330	TCC Ser	TTC Phe	TCC Ser	CAG Gln	1068
AAC Asn 335	CCC Pro	TGC Cys	CTC Leu	ATG Met	GAG Glu 340	GCC Ala	ATT Ile	GCG Ala	GCT Ala	AAA Lys 345	ATG Met	CGT Arg	TTC Phe	CAC His	AGA Arg 350	1116
CAA Gln	CTC Leu	TTC Phe	TCC Ser	CAG Gln 355	GAC Asp	TGG Trp	GCG Ala	GAC Asp	TCT Ser 360	ACT Thr	TTT Phe	TCT Ser	GTG Val	ATG Met 365	CAG Gln	1164
CAG Gln	CAG Gln	AAC Asn	AGC Ser 370	AGC Ser	CCT Pro	GCT Ala	CTG Leu	AGG Arg 375	CCC Pro	CAG Gln	CTC Leu	AGG Arg	CTA Leu 380	CCC Pro	GTT Val	1212
CTG Leu	TCT Ser	TTC Phe 385	TTC Phe	ATC Ile	CTT Leu	ACC Thr	TTG Leu 390	ATT Ile	CTG Leu	CTG Leu	CAG Gln	ACC Thr 395	CTC Leu	TGG Trp		1257
TAAC	CTGGC	GCT (ссто	CAGG	T CO	CTTTC	TCCI	CTC	CAC	CACA	CCCZ	AGAC	CGA (CTTGC	CAGCCT	1317
GTG	ATGGO	GAG A	AGAA	ATG	CT GO	CCTC	TGG#	A AGA	AAGAT	rgca	ACC	AGGCT	CA (CTGC	ACATCO	1377
TGT	CTGCT	rcc A	AGATO	GAGG	rc T	rggaz	AGAAC	G CGA	AGGG	CTGT	GAC	CGTT	CAG A	AATCO	CTGAGO	1437
GGC	CAGC	TTT (CAAAC	CCTCT	rc ci	racti	PACTO	CTC	CTT	GGC	TGCT	CCT	CCC !	ragg <i>i</i>	ACCTTO	1497
TAC	CCAC	GTT T	rggci	rgtat	ra To	rgrgo	TGGT	GAT	TAGO	CTTC	CCAC	CTC	CAG	CCCTT	CTTCC	1557
TGT	TCCC	CAG (GACC	ACCC	AG GO	CTA	ATGAC	TC#	ACTC	ATTC	CTG	TTG	CT	rctco	CAGGAA	1617
GGC2	AGGCT	rga (GGGTT	rctg?	AG GO	CAGCI	rgaga	A AAC	SATGO	STCC	CTTT	rgtg?	AGG 2	AAGGG	CTGGTG	1677
GTC	CAACO	CGT (CGAC	GCGG	CC GC	2										1699

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 397 amino acids
 - (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Gly Leu Ser Arg Ser Pro Arg Pro Pro Pro Leu Val Ile Leu Leu 1 5 10 15

Leu Val Leu Ser Leu Trp Leu Pro Leu Gly Thr Gly Asn Ser Leu Pro

25 20 Thr Glu Asn Arg Leu Val Asn Ser Cys Thr Gln Ala Arg Lys Lys Cys Glu Ala Asn Pro Ala Cys Lys Ala Ala Tyr Gln His Leu Asp Ser Cys Thr Pro Ser Leu Ser Ser Pro Leu Pro Ser Gly Glu Ser Ala Thr Ser Ala Ala Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser Ser Leu Ile Asp Cys Arg Cys His Arg Arg Met Lys His Gln Ala Thr Cys Leu Asp 105 Ile Tyr Trp Thr Val His Pro Val Arg Ser Leu Gly Asp Tyr Glu Leu 120 Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro Trp Lys Met Asn Leu Ser Lys Leu Ser Met Leu Lys Pro Asp Ser Asp Leu Cys Leu 150 Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Ile Arg Cys Gln Arg His Leu Cys Leu Ala Gln Leu Arg Ser Phe Phe Glu Lys Ala Ala Glu Ser His 200 Ala Gln Gly Leu Leu Cys Pro Cys Ala Pro Glu Asp Ala Gly Cys 220 Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Ser Cys Ala Leu Pro Ser Val Ala Pro Asn Cys Leu Asp Leu Arg Ser Phe Cys Arg Ala Asp Pro 250 Leu Cys Arg Ser Arg Leu Met Asp Phe Gln Thr His Cys His Pro Met 265 Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe Ile Ser Lys 300 Val Asn Thr Thr Val Ala Leu Gly Cys Thr Cys Arg Gly Ser Gly Asn 310 Leu Gln Asp Glu Cys Glu Gln Leu Glu Lys Ser Phe Ser Gln Asn Pro Cys Leu Met Glu Ala Ile Ala Ala Lys Met Arg Phe His Arg Gln Leu Phe Ser Gln Asp Trp Ala Asp Ser Thr Phe Ser Val Met Gln Gln 360

157K /68

Asn Ser Ser Pro Ala Leu Arg Pro Gln Leu Arg Leu Pro Val Leu Ser 370 380

Phe Phe Ile Leu Thr Leu Ile Leu Leu Gln Thr Leu Trp 385 390 395

- (2) INFORMATION FOR SEQ ID NO:43:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Val Xaa Xaa Leu Xaa Xaa Xaa Pro Xaa Pro Pro Xaa Xaa Met 1 5 10 15

Gly Ala Glu Leu Xaa Gly Xaa Xaa Arg Leu Xaa Asp Cys Val Xaa 35 40 45

Ala Xaa Xaa Xaa Cys Xaa Ala Glu Xaa Xaa Cys Ser Xaa Xaa Tyr Arg 50 55 60

Thr Leu Arg Gln Cys Xaa Ala Gly Xaa Xaa Xaa Asn Thr Xaa Leu Ala 65 70 75 80

Ser Gly Xaa Glu Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Ala Xaa Glu 85 90 95

Xaa Leu Xaa Xaa Ser Ser Leu Tyr Asp Cys Arg Cys Lys Arg Gly Met 100 105 110

Lys Lys Glu Xaa Xaa Cys Leu Xaa Ile Tyr Trp Ser Xaa His Xaa Xaa 115 120 125

Leu Xaa Xaa Gly Asn Xaa Xaa Leu Glu Xaa Ser Pro Tyr Glu Pro Xaa 130 135 140

Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Xaa Xaa Ser Xaa Xaa Ser 145 150 155 160

Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Lys Ser Asn Xaa Cys Leu 165 170 175

Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Xaa Cys Lys Leu Arg 180 185 190

Ser Ala Tyr Ile Xaa Xaa Cys Xaa Xaa Xaa Xaa Ser Xaa Xaa Glu Arg 195 200 205

Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys 210 220 Val Pro Xaa Xaa His Xaa Tyr Gly Met Leu Phe Cys Ser Cys Xaa Xaa Xaa Asp Xaa Ala Cys Xaa Glu Arg Arg Arg Gln Thr Ile Xaa Pro Ser Cys Ser Tyr Glu Xaa Xaa Glu Lys Pro Asn Cys Leu Asp Leu Arg Xaa Xaa Cys Arg Thr Asp Xaa Leu Cys Arg Ser Arg Leu Ala Asp Phe Xaa Thr Asn Cys Xaa Xaa Xaa Xaa Arg Xaa Val Xaa Ser Cys Xaa Ala Xaa Asn Tyr Xaa Xaa Cys Leu Xaa Ala Tyr Xaa Gly Leu Ile Gly Thr Xaa Met Thr Pro Asn Tyr Val Asp Ser Ser Xaa Thr Xaa Xaa Xaa Val Ala Pro Trp Cys Xaa Cys Arg Gly Ser Gly Asn Xaa Xaa Glu Glu Cys Glu Lys Phe Leu Xaa Phe Phe Xaa Xaa Asn Pro Cys Leu Xaa Asn Ala Ile Xaa Pro Xaa Phe Ser Val Xaa Xaa Xaa Xaa Thr Xaa Thr Xaa Ala Xaa Arg Val Xaa Xaa Xaa Pro Ser Leu Xaa Xaa Xaa Xaa Ser Xaa Xaa 410 Xaa Xaa Leu Xaa Thr Xaa Val Xaa Xaa Xaa Cys Xaa Xaa Leu Gln Xaa 425 Gln Xaa Leu Lys Xaa Asn Xaa Ser Xaa Glu Xaa Xaa Xaa Cys Phe Xaa 440 Glu Leu Thr Thr Asn Xaa Xaa Xaa Ser Gly Xaa Xaa Xaa Ile 455 Xaa Xaa Xaa Ser Xaa Xaa Ala Xaa Pro Ser Xaa Ala Leu Xaa Xaa Leu Pro Val Leu Met Leu Thr Ala Leu Ala Xaa Leu Leu Ser Xaa Xaa Xaa 490 485

Xaa Ser

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 489 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi)	SEQU	JENCI	E DES	CRIE	OITS	1: SE	EQ II	ON C	44:						
Xaa 1	Xaa	Xaa	Xaa	Xaa 5	Xaa	Xaa	Xaa	Xaa	Pro 10	Xaa	Xaa	Xaa	Xaa	Leu 15	Xaa
Thr	Leu	Xaa	Ser 20	Leu	Xaa	Xaa	Pro	Leu 25	Xaa	Leu	Xaa	Xaa	Ser 30	Xaa	Xaa
Xaa	Xaa	Xaa 35	Arg	Xaa	Xaa	Xaa	Asp 40	Cys	Val	Xaa	Ala	Xaa 45	Xaa	Xaa	Cys
Xaa	Ala 50	Glu	Xaa	Xaa	Cys	Ser 55	Xaa	Xaa	Tyr	Arg	Thr 60	Leu	Arg	Gln	Cys
Xaa 65	Ala	Gly	Xaa	Xaa	Xaa 70	Asn	Xaa	Xaa	Xaa	Xaa 75	Xaa	Xaa	Xaa	Xaa	Ala 80
Xaa	Xaa	Glu	Cys	Xaa 85	Xaa	Ala	Xaa	Glu	Xaa 90	Leu	Xaa	Xaa	Ser	Ser 95	Leu
Tyr	Asp	Cys	Arg 100	Cys	Lys	Arg	Gly	Met 105	Lys	Lys	Glu	Xaa	Xaa 110	Cys	Leu
Xaa	Ile	Tyr 115	Trp	Ser	Xaa	His	Xaa 120	Xaa	Leu	Xaa	Xaa	Gly 125	Xaa	Xaa	Xaa
Leu	Glu 130	Xaa	Ser	Pro	Tyr	Glu 135	Xaa	Pro	Val	Thr	Ser 140	Arg	Leu	Ser	Asp
Ile 145	Phe	Arg	Xaa	Xaa	Ser 150	Xaa	Xaa	Ser	Xaa	Xaa 155	Xaa	Xaa	Asp	Xaa	Xaa 160
Xaa	Xaa	Xaa	Lys	Ser 165	Asn	Xaa	Cys	Leu	Asp 170	Ala	Ala	Lys	Ala	Cys 175	Asn
Leu	Asn	Asp	Xaa 180	Cys	Lys	Lys	Leu	Arg 185	Ser	Ala	Tyr	Ile	Xaa 190	Xaa	Cys
Xaa	Xaa	Xaa 195	Xaa	Ser	Xaa	Xaa	Glu 200	Arg	Cys	Asn	Arg	Arg 205	Lys	Cys	His
Lys	Ala 210	Leu	Arg	Gln	Phe	Phe 215	Asp	Lys	Val	Pro	Xaa 220	Xaa	His	Xaa	Tyr
Gly 225	Met	Leu	Phe	Cys	Ser 230	Cys	Xaa	Xaa	Xaa	Asp 235	Xaa	Ala	Cys	Xaa	Glu 240
Arg	Arg	Arg	Gln	Thr 245	Ile	Xaa	Pro	Ser	Cys 250	Ser	Tyr	Glu	Xaa	Xaa 255	Glu
Xaa	Pro	Asn	Cys 260	Leu	Asp	Leu	Arg	Ser 265	Xaa	Cys	Arg	Thr	Asp 270	Xaa	Leu
Cys	Arg	Ser 275	Arg	Leu	Ala	Asp	Phe 280	Xaa	Thr	Asn	Cys	Xaa 285	Pro	Xaa	Xaa
Arg	Xaa 290	Xaa	Thr	Xaa	Cys	Xaa 295	Ala	Xaa	Asn	Tyr	Xaa 300	Xaa	Cys	Leu	Xaa
Ala 305	Tyr	Xaa	Gly	Leu	Ile 310	Gly	Thr	Xaa	Met	Thr 315	Pro	Asn	Tyr	Val	Asp 320

Ser	Xaa	Xaa	Thr	Xaa 325	Xaa	Xaa	Val	Ala	Pro 330	Trp	Cys	Xaa	Cys	Arg 335	Gly
Ser	Gly	Asn	Xaa 340	Xaa	Glu	Glu	Cys	Glu 345	Lys	Phe	Leu	Xaa	Xaa 350	Phe	Xaa
Xaa	Asn	Pro 355	Суѕ	Leu	Xaa	Asn	Ala 360	Ile	Gln	Ala	Phe	Gly 365	Asn	Gly	Xaa
Asp	Val 370	Xaa	Met	Ser	Gln	Xaa 375	Xaa	Pro	Xaa	Xaa	Xaa 380	Xaa	Thr	Xaa	Ala
Xaa 385	Xaa	Xaa	Xaa	Xaa	Xaa 390	Arg	Val	Xaa	Xaa	Xaa 395	Pro	Xaa	Leu	Xaa	Xaa 400
Xaa	Xaa	Ser	Xaa	Xaa 405	Xaa	Xaa	Xaa	Xaa	Thr 410	Xaa	Val	Xaa	Xaa	Xaa 415	Cys
Xaa	Xaa	Xaa	Gln 420	Xaa	Gln	Xaa	Leu	Lys 425	Xaa	Asn	Xaa	Ser	Xaa 430	Xaa	Xaa
Xaa	Xaa	Cys 435	Xaa	Xaa	Xaa	Xaa	Xaa 440	Xaa	Xaa	Xaa	Xaa	Xaa 445	Xaa	Xaa	Xaa
Xaa	Xaa 450	Xaa	Xaa	Xaa	Xaa	Xaa 455	Xaa	Ser	Xaa	Xaa	Ala 460	Xaa	Xaa	Ser	Xaa
Xaa 465	Leu	Xaa	Xaa	Leu	Pro 470	Val	Leu	Met	Leu	Thr 475	Xaa	Leu	Xaa	Xaa	Xaa 480
Leu	Xaa	Xaa	Xaa	Leu 485	Xaa	Glu	Thr	Ser							

antin